



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E
- (ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE
- (iii) NUMBER OF SEQUENCES: 160
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Testa, Hurwitz & Thibault
  - (B) STREET: High Street Tower - 125 High Street
  - (C) CITY: Boston
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/509,359
  - (B) FILING DATE: 31-JUL-1995
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Twomey, Michael J
  - (B) REGISTRATION NUMBER: 38349
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 248-7362
  - (B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2791 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA	120
TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCCTTA GACAGCTTGG CCTGGAGGAG	180
AACACATGAA AGAAAGAACC TCAAGAGGCT TTGTTTTCTG TGAAACAGTA TTTCTATACA	240
GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT	300

GAGGACAACC	ACCTGAGCAA	TACTGTACGT	AGCCAGAATG	ACAATAGAGA	ACGGCAGGAG	360
CACAACGACA	GACGGAGCCT	TGGCCACCCT	GAGCCATTAT	CTAATGGACG	ACCCAGGGT	420
AACTCCCGGC	AGGTGGTGGA	GCAAGATGAG	GAAGAAGATG	AGGAGCTGAC	ATTGAAATAT	480
GGCGCCAAGC	ATGTGATCAT	GCTCTTTGTC	CCTGTGACTC	TCTGCATGGT	GGTGGTCGTG	540
GCTACCATTA	AGTCAGTCAG	CTTTTATACC	CGGAAGGATG	GGCAGCTAAT	CTATACCCCA	600
TTCACAGAAG	ATACCGAGAC	TGTGGGCCAG	AGAGCCCTGC	ACTCAATTCT	GAATGCTGCC	660
ATCATGATCA	GTGTCATTGT	TGTCATGACT	ATCCTCCTGG	TGGTTCTGTA	TAAATACAGG	720
TGCTATAAGG	TCATCCATGC	CTGGCTTATT	ATATCATCTC	TATTGTTGCT	GTTCTTTTTT	780
TCATTCAATTT	ACTTGGGGGA	AGTGTTTAAA	ACCTATAACG	TTGCTGTGGA	CTACATTACT	840
GTTGCACTCC	TGATCTGGAA	TTTGGGTGTG	GTGGGAATGA	TTTCCATTCA	CTGGAAAGGT	900
CCACTTCGAC	TCCAGCAGGC	ATATCTCATT	ATGATTAGTG	CCCTCATGGC	CCTGGTGTTT	960
ATCAAGTACC	TCCCTGAATG	GACTGCGTGG	CTCATCTTGG	CTGTGATTTC	AGTATATGAT	1020
TTAGTGGCTG	TTTTGTGTCC	GAAAGGTCCA	CTTCGTATGC	TGGTTGAAAC	AGCTCAGGAG	1080
AGAAATGAAA	CGCTTTTTCC	AGCTCTCATT	TACTCCTCAA	CAATGGTGTG	GTTGGTGAAT	1140
ATGGCAGAAG	GAGACCCGGA	AGCTCAAAGG	AGAGTATCCA	AAAATTCCAA	GTATAATGCA	1200
GAAAGCACAG	AAAGGGAGTC	ACAAGACACT	GTTGCAGAGA	ATGATGATGG	CGGGTTCAGT	1260
GAGGAATGGG	AAGCCCAGAG	GGACAGTCAT	CTAGGGCCTC	ATCGCTCTAC	ACCTGAGTCA	1320
CGAGCTGCTG	TCCAGGAATC	TTCCAGCAGT	ATCCTCGCTG	GTGAAGACCC	AGAGGAAAGG	1380
GGAGTAAAC	TTGGATTGGG	AGATTTTCATT	TTCTACAGTG	TTCTGGTTGG	TAAAGCCTCA	1440
GCAACAGCCA	GTGGAGACTG	GAACACAACC	ATAGCCTGTT	TCGTAGCCAT	ATTAATTGGT	1500
TTGTGCCTTA	CATTATTACT	CCTTGCCATT	TTCAAGAAAG	CATTGCCAGC	TCTTCCAATC	1560
TCCATCACCT	TTGGGCTTGT	TTTCTACTTT	GCCACAGATT	ATCTTGTACA	GCCTTTTATG	1620
GACCAATTAG	CATTCCATCA	ATTTTATATC	TAGCATATTT	GCGGTTAGAA	TCCCATGGAT	1680
GTTTCTTCTT	TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTTCC	TGTGTCCACA	1740
TCTAACAAAG	TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCTGACC	1800
ACCTTGCACT	ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTTG	AACATACTTC	1860
ATCGCAGTGG	ACTGTGTCCT	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920
GATATGATAG	CCCCGGAAGT	TGCTGTGCCC	CATCAGCAGC	TTGACGCGTG	GTCACAGGAC	1980
GATTTCACTG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040
TTTAAACCAA	ACGGAATCTT	TCATCTTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100
GTATTAAC TG	AATTCTGAAC	TTTTCAGGAG	GTA CTGTGAG	GAAGAGCAGG	CACCAGCAGC	2160
AGAATGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220

CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA	2280
TGCCTTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATTT	2340
CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTTAA CCTCAGGTTG	2400
CAAATTCAGT AAATTTTGGG AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA	2460
AGTCAAATTT GGATTTTCCA CCAAATCTG AATTTGTAGA CATACTTGTA CGCTCACTTG	2520
CCCCAGATGC CTCCTCTGTC CTCATTCTTC TCTCCACAC AAGCAGTCTT TTTCTACAGC	2580
CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCTCACTT ATTCTAGGGT CTTACTCTTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn	20	25	30	
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu	35	40	45	
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCCC GGGCGCGGAG	60
AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA	120
CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC	180
TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA	240
GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA	300
GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA	360
CTCAAGACAG GTGGTGGAAc AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG	420
AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC	480
CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT	540
CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT	600
CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG	660
CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTTC	720
GTTCATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC KCCGTGGACT ACGTTACAGT	780
AGCACTCCTA ATCTGGAATT GGGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC	840
CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT	900
CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTTGGCT GTGATTTTCAG TATATGATTT	960
GGTGGCTGTT TTATGTCCCA AAGGCCCACT TCGTATGCTG GTTGAAACAG CTCAGGAAAG	1020
AAATGAGACT CTCTTTCCAG CTCTTATCTA TTCCTCAACA ATGGTGTGGT TGGTGAATAT	1080
GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA	1140
AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA	1200
GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG	1260
AGCTGCTGTC CAGGAACTTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG	1320
AGTAAAACTT GGAAGTGGGAG ATTTTCATTTT CTACAGTGTT CTGGTTGGTA AGGCCTCAGC	1380
AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTK GTAGCCATAC TGATCGGCCT	1440
GTGCCTTANA TTAATCCTGC TCGCCATTTA CAAGAAAGGG TNGCCAGCCC NCCCCATCTC	1500
CATCACCTTC GGGTTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560

CCAACCTTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC	1620
TTCTTTGATT ATCAAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT	1680
TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA	1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT	1800
CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT	1920
TACCCGCAC	1929

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Glu	Ile	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Ser	His	Ser	Ser	Ser	Ala	Ile	Arg	Ser	Gln	Asn	Asp	Ser	20	25	30	
Gln	Glu	Arg	Gln	Gln	Gln	His	Asp	Arg	Gln	Arg	Leu	Asp	Asn	Pro	Glu	35	40	45	
Pro	Ile	Ser	Asn	Gly	Arg	Pro	Gln	Ser	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Ile	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Xaa	180	185	190	

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Trp Gly Val Val  
 195 200 205  
 Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
 210 215 220  
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 225 230 235 240  
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 245 250 255  
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 260 265 270  
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 275 280 285  
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 290 295 300  
 Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala  
 305 310 315 320  
 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe  
 325 330 335  
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 340 345 350  
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile  
 355 360 365  
 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 370 375 380  
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 385 390 395 400  
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Xaa Val Ala Ile Leu Ile  
 405 410 415  
 Gly Leu Cys Leu Xaa Leu Leu Leu Leu Ala Ile Tyr Lys Lys Gly Xaa  
 420 425 430  
 Pro Ala Xaa Pro Ile Ser Ile Thr Phe Gly Phe Val Phe Xaa Phe Ala  
 435 440 445  
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln  
 450 455 460  
 Phe Tyr Ile  
 465

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA CGAGGGAAAT GCTGTTTGCT CGAAGACGTC TCAGGGCGCA GGTGCCTTGG	60
GCCGGGATTA GTAGCCGTCT GAACTGGAGT GGAGTAGGAG AAAGAGGAAG CGTCTTGGGC	120
TGGGTCTGCT TGAGCAACTG GTGAAACTCC GCGCCTCACG CCCCGGGTGT GTCCTTGTCC	180
AGGGGCGACG AGCATTCTGG GCGAAGTCCG CACSCCTCTT GTTCGAGGCG GAAGACGGGG	240
TCTGATSCCT TCTCCTTGGT CGGGMCTGTC TCGAGGCATG CATGTCCAGT GACTCTTGTG	300
TTTGCTGCTG CTTCCCTCTC AGATTCTTCT CACCGTTGTG GTCAGCTCTG CTTTAGGCAN	360
TATTAATCCA TAGTGGAGGC TGGGATGGGT GAGAGAATTG AGGTGACTTT TCCATAATTC	420
AGACCTAATC TGGGAGCCTG CAAGTGACAA CAGCCTTTGC GGTCCCTAGA CAGCTTGGCC	480
TGGAGGAGAA CACATGAAAG AAAGAACCTC AAGAGGCTTT GTTTTCTGTG AAACAGTATT	540
TCTATACAGT TGCTCCAATG ACAGAGTTAC CTGCACCGTT GTCCTACTTC CAGAATGCAC	600
AGATGTCTGA GGACAACCAC CTGAGCAATA CTAATGACAA TAGAGAACGG CAGGAGCACA	660
ACGACAGACG GAGCCTTGGC CACCCTGAGC CATTATCTAA TGGACGACCC CAGGGTAACT	720
CCCGGCAGGT GGTGGAGCAA GATGAGGAAG AAGATGAGGA GCTGACATTG AAATATGGCG	780
CCAAGCATGT GATCATGCTC TTTGTCCCTG TGACTCTCTG CATGGTGGTG GTCGTGGCTA	840
CCATTAAGTC AGTCAGCTTT TATACCCGGA AGGATGGGCA GCTAATCTAT ACCCCATTCA	900
CAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT GCTGCCATCA	960
TGATCAGTGT CATTGTTGTC ATGACTATCC TCCTGGTGGT TCTGTATAAA TACAGGTGCT	1020
ATAAGGTCAT CCATGCCTGG CTTATTATAT CATCTCTATT GTTGCTGTTT TTTTTTTCAT	1080
TCATTTACTT GGGGGAAGTG ,TTTAAACCT ATAACGTTGC TGTGGACTAC ATTACTGTTG	1140
CACTCCTGAT CTGGAATTTG GGTGTGGTGG GAATGATTTT CATTCACTGG AAAGGTCCAC	1200
TTCGACTCCA GCAGGCATAT CTCATTATGA TTAGTGCCCT CATGGCCCTG GTGTTTATCA	1260
AGTACCTCCC TGAATGGACT GCGTGGCTCA TCTTGGCTGT GATTTCAGTA TATGATTTAG	1320
TGGCTGTTTT GTGTCCGAAA GGTCCACTTC GTATGCTGGT TGAAACAGCT CAGGAGAGAA	1380
ATGAAACGCT TTTTCCAGCT CTCATTTACT CCTCAACAAT GGTGTGGTTG GTGAATATGG	1440
CAGAAGGAGA CCCGGAAGCT CAAAGGAGAG TATCCAAAAA TTCCAAGTAT AATGCAGAAA	1500
GCACAGAAAG GGAGTCACAA GACACTGTTG CAGAGAATGA TGATGGCGGG TTCAGTGAGG	1560
AATGGGAAGC CCAGAGGGAC AGTCATCTAG GGCCTCATCG CTCTACACCT GAGTCACGAG	1620
CTGCTGTCCA GGAACTTTCC AGCAGTATCC TCGCTGGTGA AGACCCAGAG GAAAGGGGAG	1680
TAAAACTTGG ATTGGGAGAT TTCATTTTCT ACAGTGTTCT GGTTGGTAAA GCCTCAGCAA	1740
CAGCCAGTGG AGACTGGAAC ACAACCATAG CCTGTTTCGT AGCCATATTA ATTGGTTTGT	1800
GCCTTACATT ATTACTCCTT GCCATTTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA	1860



TCACCTTTGG GCTTGTTTTT TACTTTGCCA CAGATTATCT TGTACAGCCT TTTATGGACC	1920
AATTAGCATT CCATCAATTT TATATCTAGC ATATTGCGG TTAGAATCCC ATGGATGTTT	1980
CTTCTTTGAC TATAACCAAA TCTGGGGAGG ACAAAGGTGA TTTTCCTGTG TCCACATCTA	2040
ACAAAGTCAA GATTCCCGGC TGGACTTTTG CAGCTTCCTT CCAAGTCTTC CTGACCACCT	2100
TGCACTATTG GACTTTGGAA GGAGGTGCCT ATAGAAAACG ATTTTGAACA TACTTCATCG	2160
CAGTGGACTG TGTCTCGGT GCAGAACTA CCAGATTGA GGGACGAGGT CAAGGAGATA	2220
TGATAGGCCC GGAAGTTGCT GTGCCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT	2280
TCCTGACAC TGCGAACCTC CAGGACTACC GGTTACCAAG AGGTTAGGTG AAGTGGTTTA	2340
AACCAAACGG AACTCTTCAT CTTAACTAC ACGTTGAAA TCAACCCAAT AATTCTGTAT	2400
TAAGTGAATT CTGAACTTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA	2460
TGGGGAATGG AGAGGTGGGC AGGGGTTCCA GCTTCCCTTT GATTTTTTGC TGCAGACTCA	2520
TCCTTTTTTA ATGAGACTTG TTTTCCCTC TCTTTGAGTC AAGTCAAATA TGTAGATGCC	2580
TTTGGCAATT CTTCTTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTTCTTC	2640
CCAAGGCCAG TCTGAACCTG AGGTTGCTTT ATCCTAAAAG TTTTAACCTC AGGTTCCAAA	2700
TTCAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTTGAAGTC	2760
AAATTTGGAT TTTCCACCAA ATTCTGAATT TGTAGACATA CTTGTACGCT CACTTGCCCC	2820
AGATGCCTCC TCTGTCTCTA TTCTTCTCTC CCACACAAGC AGTCTTTTTT TACAGCCAGT	2880
AAGGCAGCTC TGTCGTGGTA GCAGATGGTC CCACTTATTC TAGGGTCTTA CTCTTTGTAT	2940
GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTTCCACA	3000
GCAAATGAGA TGTATGCCCA AAGCGGTAGA ATTAAAGAAG AGTAAAATGG CTGTTGAAGC	3060
AAAAAAAAAA AAAAAAAAAA AAAAAA	3087

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240

TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT	300
TGTACATCTT TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTG TGATTAGTGC	480
CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTTCA GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC	600
ACTGGAGTGT TTTCTTTCTT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAAAT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG	CTTCACGGGG	GAGGCTGTGC	GGGAAGAATG	CTCCACACA	GNATAAGAA	60
TGCTCCCGCA	CAGGATAGAG	AATGCCCCCG	CACAGCATAG	AGAAGCCCCC	GCACAGCATA	120
GAGAATGCCC	CCNCACAGCA	TAGAGAAGCC	CCCGCACAGC	ATAGAGAATG	CTCTTCACCT	180
CTGGGTTTTT	AACCAGCCAA	ACTAAAATCA	CAGAGGSCMA	CACATCATTT	AAGATAGAAA	240
TTTCTGTATC	TTTAAATTTY	TTTCMAAGTA	GTTTTACTTA	TTTTCAGATT	CTATTTCTTT	300
ACTAGAATTA	AGGGATAAAA	TAACAATGTG	TGCATAATGA	ACCCTATGAA	ACMAACMMAA	360
GCTAGGTTTT	TTTCATAGST	CTTCTTCCAG	ATTGAATGAA	CGTCTGTTCT	AAAATTTAAC	420
CCCCCAGGGA	AATATTCAGT	TAATATGTT	AAAAACCCAG	ACTTGTGATT	GAGTTTTGCC	480
TGAAAATGCT	TTCATAATTA	TGTGTGAATG	TGTGTC			516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC	CCTTTTTAGA	CCATACAAGG	TAACTTCCGG	ACGTTGCCAT	GGCATCTGTA	60
AACTGTCATG	GTGTTGGCGG	GGAGTGTCTT	TTAGCATGCT	AATGTATTAT	AATTAGCGTA	120
TAGTGAGCAG	TGAGGATAAC	CAGAGGTCAC	TCTCCTCACC	ATCTTGTTTT	TGGTGGGTTT	180
TGGCCAGCTT	CTTTATTGCA	ACCAGTTTTA	TCAGCAAGAT	CTTTATGAGC	TGTATCTTGT	240
GCTGACTTCC	TATCTCATCC	CGNAACTAAG	AGTACCTAAC	CTCCTGCAA	TTGMAGNCCA	300
GNAGGTCTTG	GNCTTATTTN	ACCCAGCCCC	TATTCAARAT	AGAGTNGYTC	TTGGNCCAAA	360
CGCCYCTGAC	ACAAGGATTT	TAAAGTCTTA	TTAATTAAGG	TAAGATAGKT	CCTTGSATAT	420
GTGGTCTGAA	ATCACAGAAA	GCTGAATTTG	GAAAAAGGTG	CTTGGASCTG	CAGCCAGTAA	480
ACAAGTTTTC	ATGCAGGTGT	CAGTATTTAA	GGTACATCTC	AAAGGATAAG	TACAATTGTG	540
TATGTTGGGA	TGAACAGAGA	GAATGGAGCA	ANCCAAGACC	CAGGTAAAAG	AGAGGACCTG	600
AATGCCTTCA	GTGAACAATG	ATAGATAATC	TAGACTTTTA	AACTGCATAC	TTCCTGTACA	660
TTGTTTTTTC	TTGCTTCAGG	TTTTTAGAAC	TCATAGTGAC	GGGTCTGTTG	TTAATCCCAG	720
GTCTAACCGT	TACCTTGATT	CTGCTGAGAA	TCTGATTTAC	TGAAAATGTT	TTTCTGTGTC	780
TTATAGAATG	ACAATAGAGA	ACGGCAGGAG	CACAACGACA	GACGGAGCCT	TGGCCACCCT	840

GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTCTTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCCTTNC TNACTTKGGN GGATTAAATT	1380
CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTTG GGACAAGGGA GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCCNGCT GNTGTGTNCT NCCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCTT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTCNCCAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCCTGG AGACCATATG ACCCATAGAG CTTAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTTCTG ACTTTGTAA TAGAAAATCA ACCCAACTGG TTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTACAGTTC	360
ATCCAAGGAC TCAATCTCCT TCTTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480
ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600

CTKKNTGGCT	GGGAATATTG	GCACCTGGAA	TAAAAATGTT	TTTCTGTGAA	TGAGAAACAA	660
GGGGAAGATG	GATATGTGAC	ATTATCTTAA	GACAACTCCA	GTTGCAATTA	CTCTGCAGAT	720
GAGAGGCACT	AATTATAAGC	CATATTACCT	TTCTTCTGAC	AACCACTTGT	CAGCCNCNGT	780
GGTTTCTGTG	GCAGAATCTG	GTTCYATAMC	AAGTTCCTAA	TAANCTGTAS	CCNAAAAAAT	840
TTGATGAGGT	ATTATAATTA	TTTCAATATA	AAGCACCCAC	TAGATGGAGC	CAGTGTCTGC	900
TTACATGTT	AAGTCCTTCT	TTCCATATGT	TAGACATTTT	CTTTGAAGCA	ATTTTAGAGT	960
GTAGCTGTTT	TTCTCAGGTT	AAAAATTCTT	AGCTAGGATT	GGTGAGTTGG	GGAAAAGTGA	1020
CTTATAAGAT	NCGAATTGAA	TTAAGAAAAA	GAAAATTCTG	TGTTGGAGGT	GGTAATGTGG	1080
KTGGTGATCT	YCATTAAACAC	TGANCTAGGG	CTTTKKGKGT	TGKTTTATTG	TAGAATCTAT	1140
ACCCCATTC	NAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	1200
GCTGCCATCA	TGATCAGNGT	CATTGTWGTG	ATGACTANNC	TCCTGGTGGT	TCWGTATAAA	1260
TACAGGTGCT	ATAAGGTGAG	CATGAGACAC	AGATCTTTGN	TTCCACCCT	GTTCTTCTTA	1320
TGGTTGGGTA	TTCTTGTCAC	AGTAACTTAA	CTGATCTAGG	AAAGAAAAAA	TGTTTTGTCT	1380
TCTAGAGATA	AGTTAATTTT	TAGTTTTCTT	CCTCCTCACT	GTGGAACATT	CAAAAAATAC	1440
AAAAAGGAAG	CCAGGTGCAT	GTGTAATGCC	AGGCTCAGAG	GCTGAGGCAG	GAGGATCGCT	1500
TGGGCCCAGG	AGTTCACAAG	CAGCTTGGGC	AACGTAGCAA	GACCCTGCCT	CTATTAAAGA	1560
AAACAAAAAA	CAAATATTGG	AAGTATTTTA	TATGCATGGA	ATCTATATGT	CATGAAAAAA	1620
TTAGTGTA	ATATATATAT	TATGATTAGN	TATCAAGATT	TAGTGATAAT	TTATGTTATT	1680
TTGGGATTT	AATGCCTTTT	TAGGCCATTG	TCTCAAMAAA	TAAAAGCAGA	AAACAAAAAA	1740
AGTTGTAACT	GAAAAATAAA	CATTTCATA	TAATAGCACA	ATCTAAGTGG	GTTTTTGNTT	1800
GTTTGTGTT	TTGTTGAAGC	AGGGCCTTGC	CCTNYCACCC	AGGNTGGAGT	GAAGTGCAGT	1860
GGCACGATTT	TGGCTCACTG	CAG				1883

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 823 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGGA	CTAGGTAAAT	GNAAGNTGTT	TTAAAGAGAG	ATGNGGNCNG	GGACATAGTG	60
GTACACANCT	GTAATGCTCA	NCACTKATGG	GGAGTACTGA	AGGNGGNSGG	ATCACTTGNG	120
GGTCNGGAAT	NTGAGANCAG	CCTGGGCAAN	ATGGCGAAAC	CCTGTCTCTA	CTAAAAATAG	180

CCANAAWNWA	GCCTAGCGTG	GTGGCGCRCA	CGCGTGGTTC	CACCTACTCA	GGAGGCNTAA	240
GCACGAGNAN	TNCTTGAACC	CAGGAGGCAG	AGGNTGTGGT	GARCTGAGAT	CGTGCCACTG	300
CACTCCAGTC	TGGGCGACMA	AGTGAGACCC	TGTCTCCNNN	AAGAAAAAAAA	AAATCTGTAC	360
TTTTTAAGGG	TTGTGGGACC	TGTTAATTAT	ATTGAAATGC	TTCTYTTCTA	GGTCATCCAT	420
GCCTGGCTTA	TTATATCATC	TCTATTGTTG	CTGCTCTTTT	TTACATTCAT	TTACTTGGGG	480
TAAGTTGTGA	AATTTGGGGT	CTGTCTTTCA	GAATTAACTA	CCTNNGTGCT	GTGTAGCTAT	540
CATTTAAAGC	CATGTACTTT	GNTGATGAAT	TACTCTGAAG	TTTAAATTGT	NTCCACATAT	600
AGGTCATACT	TGGTATATAA	AAGACTAGNC	AGTATTACTA	ATTGAGACAT	TCTTCTGTNG	660
CTCCTNGCTT	ATAATAAGTA	GAAGTAAAAG	NAACTTAAGA	CTACAGTTAA	TTCTAAGCCT	720
TTGGGGAAGG	ATTATATAGC	CTTCTAGTAG	GAAGTCTTGT	GCNATCAGAA	TGTTTNTAAA	780
GAAAGGGTNT	CAAGGAATNG	TATAAANACC	AAAAATAATT	GAT		823

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTTCCCA	TCTTCTCCAC	AGAGTTTGTG	CCTTACATTA	TTACTCCTTG	CCATTTTCAA	60
GAAAGCATTG	TCAGCTCTTC	CAATCTCCAT	CACCTTTGGG	CTTGTTTTCT	ACTTTGCCAC	120
AGATTATCTT	GTACAGCCTT	TTATGGACCA	ATTAGCATTC	CATCAATTTT	ATATCTAGCA	180
TATTTGCGGT	TAGAATCCCA	TGGATGTTTC	TTCTTTGACT	ATAACAAAAT	CTGGGGAGGA	240
CAAAGGTGAT	TTCCTGTGTC	CACATCTAAC	AAATCAAGAT	CCCCGGCTGG	ACTTTTGGAG	300
GTTCCTTCCA	AGTCTTCCTG	ACCACCTTGC	ACTATTGGAC	TTGGAAGGA	GGTGCCTATA	360
GAAAACGATT	TTGAACATAC	TTCATCGCAG	TGGACTGTGT	CCTCGGTGCA	GAAACTACCA	420
GATTTGAGGG	ACGAGGTCAA	GGAGATATGA	TAGGCCCGGA	AGTTGCTGTG	CCCCATCAGC	480
AGCTTGACGC	GTGGTCACAG	GACGATTTTC	ACTGACACTG	CGAACTCTCA	GGACTACCGT	540
TACCAAGAGG	TTAGGTGAAG	TGGTTTAAAC	CAAACGGAAC	TCTTCATCTT	AAACTACACG	600
TTGAAAATCA	ACCCAATAAT	TCTGTATTAA	CTGAATTCTG	AACTTTTCAG	GAGGTACTGT	660
GAGGAAGAGC	AGGCACCACC	AGCAGAATGG	GGAATGGAGA	GGTGGGCAGG	GGTTCAGCT	720
TCCCTTTGAT	TTTTTG					736

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTCAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAAAGG TTTGTTTCTG CTTAATGTAA TCTATGGAAG TGTTTTTTAT AACAGTATAA	720
TTGTAGTGCA CAAAGTTCTG TTTTCTTTC CCTTTTCAGA ACCTCAAGAG GCTTTGTTTT	780
CTGTGAAACA GTATTTCTAT ACAGTNTGCT CCAANTGNAC AGAGTTACCT GCACNNCGTT	840
GTCCNTACTT CCAGAATGCA CAGATGTCTG AGGACAACCA CCTGAGCAAT ACT	893

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA CTTTNGGGCA CATGAGAATC ACATGAGAAC AAGCTGATGC ATAATTCCTC	60
CTGTGATGGA ATGTAATAGT AATTTAACAG TGTCTTTTCT TTTTAACTGC CTCAAGGATA	120
CAGCAAAATA AAACAAAAGC AATATGAAGG CTGAGAATAG GTATCAGATT ATCATAAAAA	180

GTATAGATCA AAAGGAATCT GGTKCTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG	240
GAGACTTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCCAGG RAAACTTGAT	300
ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC	360
ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNGGAAATAC CTGGRAGGTT	420
ACTGAAAGGC NACNATCAGA CNAATAATAA GNATACCGTA GGTAAATTCT ACAGT	475

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCTCNAGA TCTCTTCAAA ATTCATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC	60
TGGAACCAGA CTTGCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA	120
TTTACAGGGG GCTCGTAAAG AATCCTGTTT TGANTATTNT NCCGTCAATT ACCNCCCCAA	180

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTTNC	60
TTTTTNCACCT CTCAGACATA AATATAAACM MANTTTCTAC TGTGGRAAAA CATCTNCAGG	120
GGNCNTTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTTAAT GTCTCTAAGC	180
NACTNGACTA GTTTCTCTTN CACTGAGNAA ACTGCNACAA GTNNTTNCTN CTGNATCTGN	240
ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA	300
GTNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT	360
CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA	420
TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT	457



(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 373 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT	60
AAGTCATTCG CTNTGANCNA CACATAACAG ATCTCGCAAC TGNAGTTTAG CGAGGCCAGT	120
TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCMAA GTCCNACTGT	180
TTAGTCAAGA GACCCTACTG TTAAC TAGTA CCTTTACACT ACTAACTGGG TAANCCATAA	240
NCAATTAATG ATAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAAACNT	300
CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTAT TAGGATAAAC TTCAAGNAG	360
TGGATNCTAG GTG	373

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 422 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCCAC	60
AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGGCCAATC AGATCCTACC	120
TCCANGGGGT TNGGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA	180
GGGCCCATAC ATTCAGGAGC CTTATGGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG	240
GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTTCCTGT TTCCCAATGN TAAGTCCCTG	300
CCATGTYCCT GCTCTTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG	360
GCCCTGGCAG CTTTTCAAAT CCTYCCCAT TTTATTGAAG CTGAAAGACC CTTGACTAGA	420
AC	422

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT TTCGTCACTA CCTCCCCGGG TCGGGAGTGG GTAATTTGCG CGCCTGCTGC	60
CTTCCTTGGA TGTGGTAGCC GTTCTCAGG CTCCCTCTCC GGAATCGAAC CCTGATTCCC	120
CGTCACCCGT GGTCAACATG GTTAGGCACG GCGACTACCA TCGAAAGTTA ATAGGGCAGA	180
TCTCGAGAAT TCTCGAGATC TCCNTCMAAT TATTACTTCA NTKCGGTAG TGATCAGNAC	240
NAGGCAGTTC TATTGATTTC TCTCCTTCA TTCTGAGTTT CTCCATAAAT TAATTGGACC	300
TAATCATGTT TKNAATCCTG TCTTTTAGGG GGNANTTGA CTNTCAAGTG TTTAAAGGGA	360
GGGNCGGAGN ATGATTNTGG ATTGGAGTGA GAGCA	395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTTCT GGGTNAAG GACCTNANAC ATAATATAGT GGAATTNCAA TAAACACTTA	60
CCAAATGGAN AAATGAACCC CTGGTCACCC CGATCTCACT AGTNCCTNCC CTGAAACCCG	120
ANANATCTGA GTCCTTTTCT CCTTTACTAA CCCTTNCTCC AATCCTGCTC ATGGGAATTA	180
ANGNTGTAAA ATANGCCTGG GGNACCTCGG RCCTCTNCCC TGGGNTCTGT GGGTGGGAGN	240
ACTGTGGAAG CCGTWTCAAT CGCCCCACC TATGAGAGCC TTTCTNCAGG GCCAGCCATG	300
AACGTCCCC ATGTNATCAG NATCTNCAGG CTA CTGCTGT CCTTCYTGA TWTTTAACCT	360
GGRGGCGGGC CAGGGACAGA AAARGGAGGT GGCAAGATCC TTGAACAAAA GGAGCTATAA	420
AAGGGCGTTG GGGGAAGCAA GGCAACGGC AGATTAAACA AGCAGGCACC TCAAGGAAAC	480
GTGACGC	487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT GGCCCATCAT TTAGTTTTAT NGCTTGNAGT NTNTAGNAGA TAAACATCC	60
ACGTGGATCT NCTCTTAGAG AAATCAANTA CTTTAGGNAT NTGATAGTCA GAGANTGGNT	120
ATCAAATNGA AAGGNATNTN GGTNGANCAG TTAGTTNGYN CCNTTNGNNG AGACCACTGG	180

GNTGTNGASA CCAGATTCMK GGGTNCNAAT CTTANGGTAA TCTNAGAGCC AACACATGGG	240
TCATNTTATS CCCCAAACCTT AGCCACATCT BGTGGGGYTA TGGNGTCACC CCAAGAGCAG	300
GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAATT CTGAATGNAT	360
CACCTGTTAG AGTTTCTTGT YCATAAAATA GCAGGGAATT TAGGAATTTA GTTTTTTTTT	420
AATAGTTTGG GCCTTTTATC CACACTCTCA GGAGCTTAGG ATACTTTTCT CCTTCAGCTC	480
ACTCTGAAAC TCCCTCTGGA	500

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA	60
AATAAATTTA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTTAAA	120
GGACTCMAGA GTTNCAGRNA AGTAAAAAGR AAAGAGTAAA ATCATTCTTCT AANTYTYWYY	180
TTCCAGAAAT AACGATGTTG AGCATTAAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA	240
TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG	300
CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATTT NNANTTTANA	360
AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA	406

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAACC	60
CGGATTTTAT CATGAGGGCA TTAGTGGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG	120
GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG	180
CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC	240
CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGACTTCCAC AGCAAGGTC	289

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTACTGAGTA AAAATCTCAG GTNTTAACCA TGCCCCTAAA ATGTGCTATN	60
CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT GGGNAACTCC CCNCAAATGT	120
TTATTTTAAA TAAAAATGGT NGATGGAAAT ATTTTNTAAA AGAACTTGGG GTNTAATATG	180
GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT TCCCATTAT AATAAGTTNC	240
CCACCCTTTA CTATCAAGAT TACAACTTAT TGACCTTTTA TGCTNGCTNG GTTTTTTTGG	300
GACTGCCTAA TCCAATGTTT AAATTTTCTA NGTCTGNATT TCAATGTGGG TAGGAGTNAT	360
TTTTCAA	367

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA CAGGTAAGAT TGCTTTTTTAA AGTTGTTTTA AATGCATTAC ATGACTGAGA	60
AAAGAAAAAT GCACATTTTA TTGTTGCAGT TTAAAATTTT ATTTNGNGTG AAATAAACG	120
TGAAACAAAA GGGATAAATG TGTTTTGNNT TTGTTTTGGT TTTACCTGTT TGGGGTATTT	180
TTTTCTGAGT TTGTGTAGAA ACCCGTGTGG NTACACTGGG TAATCTTGTC AGGGNTACMA	240
AMCTTGGGTC TTGANTTTGG TTANTTGGNT TTANTTGGTG NACCCATGTA CTTGCTCTTC	300
CNTCCCAGAA ACATAGCTTG GTAGGCNAGG GTTAANCCAG TGTCGGCGAN CCCATGTCCC	360
TANCACAGCA TCTTGTAAGT TTAATGCACA ATCGTTCCNT CCCAGGATGG ANTTATCATT	420
ATAAA	425

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCGCA	GGAGCCACAA	ATAAAGCAAG	AGCCAGAATC	AGAAGNGGAG	GAAGAAGAAA	60
AGCAAGAAAA	AGRAGRAANA	CGAGAAGAAC	CCATGGRAGA	GGAAGAGGAN	CCAGANCMMA	120
AGCCTTGTCT	GAAACCTACT	CTGAGGCCCA	TCAGCTCTGC	TCCATCTGTT	TCCTCTGCCA	180
GTGGNAATGC	NACACCTAAC	ACTCCTGGGG	ATGAGTCTCC	CTGTGGTATT	ATTATTCCTC	240
ATGRAAACTC	ACCAGATCAA	CAGCAACCTG	AGGAGCATAG	GCCMAAAATA	GGACTAAGTC	300
TTAAACTGGG	TGCTTCCAAT	AGTCCTGGTC	AGCCTAATTC	TGTGAAGAGA	AAGAACTAC	360
CTGTAGATAG	TGTCTTTAAC	AAATTTGAGG	ATGAAGACAG	TGATGACGTA	CCCCGAAAAA	420
GGAAACTGGT	TCCCTTGGAT	TATGGTGAAG	ATGATAAAAA	TNCAACCAAA	GGCACTGTAA	480
ACACTGAAGA	AAAGCGTAAA	CACATTAAGA	GTCTCATTGA	GAAATCCCT	ACAGCCAAAC	540
CTGAGCTCTT	CGCTTATCCC	CTGGATTGGT	CTATTGTGGA	TTCTATACTG	ATGGAACGTC	600
GAATTAGACC	ATGGATTAAT	AAGAAAATCA	TAGAATATAT	AGGTGAAGAA	GAAGCTACAT	660
TAGTTGATTT	NGTTTGTTCT	AAGGTTATGG	CTCATAGTNC	ACCCAGAGC	ATTTTAGATG	720
ATGTTGCCAT	GGTACTTGAT	GAAGAAGCAG	AAGTTTTTAT	AGTCAAAATG	TGGAGATTAT	780
TGATATATGA	AACAGAAGCC	AAGAAAATTG	GTCTTG TGAA	GTAAACTTT	TTATATTTAG	840
AGTTCCATTT	CAGATTTCTT	CTTTGCCACC	CTTTTAAGGA	CTTKGAATTT	TTCTTTGTCT	900
TKGAAGACAT	TGTGAGATCT	GTAATTTTTT	TTTTTTGTAG	AAAATGTGAA	TTTTTTGGTC	960
CTCTAATTTG	TTGTTGCCCT	GTGTACTCCC	TTGGTTGTAA	AGTCATCTGA	ATCCTTGGTT	1020
CTCTTTATAC	TCACCAGGTA	CAAATTACTG	GTATGTTTTA	TAAGCCGCAG	CTACTGTACA	1080
CAGCCTATCT	GATATAATCT	TGTTCTGCTG	ATTTGTTTCT	TGTAAATATT	AAAACGACTC	1140
CCCAATTATT	TTGCAGAATT	GCACTTAATA	TTGAAATGTA	CTGTATAGGA	ACCAACATGA	1200
ACAATTTTAA	TTGAAAACAC	CAGTCATCAA	CTATTACCAC	CCCCACTCTC	TTTTCATCAG	1260
AAATGGCAAG	CCCTTG TGAA	GGCATGGAGT	TTAAAATTGG	AATGCAAAAA	TTAGCAGACA	1320
ATCCATTCCCT	ACTGTATTTT	TGTATGAATG	TGTTTG TGAA	TGTATGTGTA	AAAGTCTTTC	1380
TTTTCCCTAA	TTTGCTTTGG	TGGGGTCCTT	AAAACATTTT	CCAATAAAG	AATAGAATTG	1440
TAAAGGAAAA	GTGGTACTGT	TCCAACCTGA	AATGTCTGTT	ATAATTAGGT	TATTAGTTTC	1500
CCAGAGCATG	GTGTTCTCGT	GTCGTGAGCA	ATGTGGGTTG	CTAACTGTAT	GGGGTTTTCT	1560
TATTAATAAG	ATGGCTGCTT	CAGCTTCTCT	TTTAAAGGAA	TGTGGATCAT	AGTGATTTTT	1620
CCTTTTAATT	TTATTGCTCA	GAAATGAGGC	ATATCCCTAA	AAATCTCGGA	GAGCTGTATT	1680
TAATGCATTT	TTGCACTAAT	TGGTCCTTAG	TTTAATTCTA	TTGTATCTGT	TTATTTAACA	1740
AAAAATTCAT	CATATCAAAA	AGTGTAAGTG	AAAACCCCTT	TTAAAACAAA	ACAAAAAAAT	1800
GAAATAAAAT	TAGGCAAATT	GACAGACAGT	GAGAGTTTTA	CAAACATGAT	AGGTATTCTG	1860
CTCGGCAATT	TGTAAGTTTA	CATGTTATTT	AAGGATAAAG	GTAAATCATT	CAAGGCAGTT	1920

ACCAACCACT AACTATTTGT TTTCATTTTT GTCTTGTAGA AGGTTTATAT CTTGTTTTAC	1980
CTTGGCTCAT TAGTGTTTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT	2040
TCTTCGTTGT AGATCAGAAT TTCACCAGGG AGTAAATTA CCTGAAAACG TAAGAAGTTT	2100
TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCAT GTCTGAGGTA CTTATTTAAA	2160
AGAAAGGTAA AGATTGGCCT GTTAGAAAA GCATAATGTG AGCTTTGGAT TACTGGATTT	2220
TTTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAC ACTGTTCTTA CCCTCGAACC	2280
CTGATGTGGT TCCATTATGT AAATATTTCA AATATTAAAA ATGTATATAT TTGAAAAAA	2340
AAAAAAAAAA AAAATTCCTG CGGCCGCAAG GGAATTC	2377

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 489 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCCC GGGCTGCAGG	60
AATTCTCGAG ATCTCCCCCA AGTAAATGAA TGAAAAAAG AACAGCAACA ATAGAGATGA	120
TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCTGTA TTTATACAGA ACCACCAGGA	180
GGATAGTCAT GACAACNATG AACTGATCA TGATNCCAGC ATTCAGAATT GAGTNCAGGG	240
CTCTCTGGCC CACAGTCTCG GTATCTTCTG TGNATGGGGT ATAGATTARC TGTCCATCCT	300
TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC	360
ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT	420
CTTCTTCCTC ATCTTNTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT	480
AATGGCTCA	489

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2307 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTTCT TCATCCTACC	60
ACAAAATCCC AGTTGGTAAT AGAGACTTTA CTCCTACCTA TCAAAACCAC AAAATGTCCC	120
ATTAGGGGGG GACATGTTGT ACATGTTAGG ATCATTCAAA TAACCAAGAT TATAAGGTGA	180

GGAAAGATGC CCCTAACTGA TTCTTTTGTC TCTCATCTTG TTGGTTCCAG GGACCGAGTG	240
GGGTCAATCT TCTGGTSSTG CCTCTCCAGG TCTCTTCCAG GCCGGTCATA GACGTACTCC	300
CTCTGAGGCC GACCGATGGT TAGAAGAGGT GTCTAAGAGC GTCCGGGCTC AGCAGCCCCA	360
GGCCTCAGCT GCTCCTCTGC AGCCAGTTCT CCAGCCTCCT CCACCCACTG CCATCTCCCA	420
GCCAGCATCA CCTTTCCAAG GGAATGCATT CCTCACCTCT CAGCCTGTGC CAGTGGGTGT	480
GGTCCCAGCC CTGCAACCAG CCTTTGTCCC TGCCCAGTCC TATCCTGTGG CCAATGGAAT	540
GCCCTATCCA GCCCCTAATG TGCCTGTGGT GGGCATCACT CCCTCCCAGA TGGTGGCCAA	600
CGTWTTTGGC ACTGCAGGCC ACCCTCAGGC TGCCCATCCC CATCAGTCAC CCAGCCTGGT	660
CAGGCAGCAG ACATTCCCTC ACTACGAGGC AAGCAGTGCT ACCACCAGTC CCTTCTTTAA	720
GCCTCCTGCT CAGCACCTCA ACGGTTCTGC AGCTTTCAAT GGTGTAGATG ATGGCAGGTT	780
GGCCTCAGCA GACAGGCATA CAGAGGTTCC TACAGGCACC TGCCCAGTGG ATCCTTTTGA	840
AGCCCAGTGG GCTGCATTAG AAAATAAGTC CAAGCAGCGT ACTAATCCCT CCCCTACCAA	900
CCCTTTCTCC AGTGACTTAC AGAAGACGTT TGAAATTGAA CTTTAAGCAA TCATTATGGC	960
TATGTATCTT GTCCATACCA GACAGGGAGC AGGGGGTAGC GGTCAAAGGA GCMAAACAGA	1020
YTTTGTCTCC TGATTAGTAC TCTTTTCACT AATCCCAAAG GTCCCAAGGA ACAAGTCCAG	1080
GCCCAGAGTA CTGTGAGGGG TGATTTTGAA AGACATGGGA AAAAGCATTG CTAGAGAAAA	1140
GCTGCCTTGC AATTAGGCTA AAGAAGTCAA GGAAATGTTG CTTTCTGTAC TCCCTCTTCC	1200
CTTACCCCCT TACAAATCTC TGGCAACAGA GAGGCAAAGT ATCTGAACAA GAATCTATAT	1260
TCCAAGCACA TTTACTGAAA TGTA AACAC AACAGGAAGC AAAGCAATGT CCCTTTGTTT	1320
TTCAGGCCAT TCACCTGCCT CCTGTCAGTA GTGGCCTGTA TTAGAGATCA AGAAGAGTGG	1380
TTTGTGCTCA GGCTGGGAAC AGAGAGGCAC GCTATGCTGC CAGAATTCCC AGGAGGGCAT	1440
ATCAGCAACT GCCCAGCAGA GCTATATTTT GGGGGAGAAG TTGAGCTTCC ATTTTGAGTA	1500
ACAGAATAAA TATTATATAT ATCAAAAGCC AAAATCTTTA TTTTATGCA TTTAGAATAT	1560
TTTAAATAGT TCTCAGATAT TAAGAAGTTG TATGAGTTGT AAGTAATCTT GCCAAAGGTA	1620
AAGGGGCTAG TTGTAAGAAA TTGTACATRA GATTGATTTA TCATTGATGC CTACTGAAAT	1680
AAAAAGAGGA AAGGCTGGAA GCATGCAGAC AGGATCCCTA GCTTGTTTTT TGTCAGTCAT	1740
TCATTGTAAG TAGCACATTG CAACAACAAT CATGCTTATG ACCAATACAG TCACTAGGTT	1800
GTAGTTTTTT TTAAATAAAG GAAAAGCAGT ATTGTCCTGG TTTTAAACCT ATGATGGAAT	1860
TCTAATGTCA TTATTTTAAT GGAATCAATC GAAATATGCT CTATAGAGAA TATATCTTTT	1920
ATATATTGCT GCAGTTTCCT TATGTTAATC CTTTAACACT AAGGTAACAT GACATAATCA	1980
TACCATAGAA GGAACACAG GTTACCATAT TGGTTTGTA TATGGGTCTT GGTGGGTTTT	2040
GTTTTATCCT TTAAATTTTG TTCCCATGAG TTTTGTGGGG ATGGGGATTC TGGTTTTATT	2100

AGCTTTGTGT GTGTCCTCTT CCCCCAAACC CCCTTTTGGT GAGAACATCC CCTTGACAGT	2160
TGCAGCCTCT TGACCTCGGA TAACAATAAG AGAGCTCATC TCATTTTAC TTTTGAACGT	2220
TGGCGCTTAC AATCAAATGT AAGTTATATA TATTTGTACT GATGAAAATT TATAATCTGC	2280
TTTAACAAAA ATAAATGTTC ATGGTAG	2307

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT TACATGGCCT CACAGGCATC AGCTGAAAAG AGGACCCMAA AAGAAATTGG	60
AGATATTGCT GGTGTTGCTG ATGTTACAAT CAGRCAGTTC TATAGACTGA TCTATCCTCG	120
AGCCCCAGAT CTGTTCTTA CAGACTTCMA ATTKGACACC CCAGTGGACA AACTACCACA	180
GCTATAAATT GAGGCAGYTA ACGTCMAATT CTTGANNACM AAACCTTKNCC TGTTGTACAT	240
AGCCTATACM AAATGCTGGG TTGAGCCTTT CATAAGGNAA AACMNAAGAC ATGGNTACGC	300
ATTCCAGGGC TKGANTACTT ATTGCTTGGC ATTCTTGAT GTA	343

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA CCAGCCACTG CACCAAAATT AGTCCTTACA TTATAATACT CTGGCCATTG	60
GAAGAGAAAA ATGGGAAAAT TCAACAATTT GAAAGACTAT GATCCCTCTG GCTCATGATC	120
TACTGACCAG AATGAAGTCC TGAAGGATTT CCTTCTGTTA TGTTATCTAC CCAGCTAATC	180
TCAAACAAGA GGAGCTGGAA AGAACAAAGC CCCATGAAGC TACCCCTAGA CCCAGAAAGC	240
CAAGAACAGG GCCAAGAAAA TGAACAGCAG ACAAGCCTGA AATAGAAGTG GNACAGACAT	300
GTGGNAAGAC CAAGTACACC CAGTTNGGTG GTAAAGATTC CGATATCAAG CTTATCGATA	360
CCG	363

(2) INFORMATION FOR SEQ ID NO:31:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTTGNCCA CCCASCAC CTTTCCCCAT CTCTACCGGY TGATAGTCTC	60
TCAGNTAGTA GACCTTTTCT NGTTTAGRCA GGGCCACNTT TTTAAAACT CCAGACGGGT	120
ACCCTCCATG TKGMAGGCGA CGTGGCCCTG GATCACTCAA CTGANTGTCA TNKGANTGGT	180
GCCCCCAGAG TGAGGACAAT GGTGNAGCCC TCCTAAGGCC CTNCCTGAGT GTCCCTCCTT	240
CATGAAGATG ATTCTGAGGN TTCCCAGGCC TNCACCCTTC TTKGAAARCC CATAGNAGTT	300
CATATGNACT NCTCTNCTAT GCTCACCAA CTCTNCCTTC ATCATACTTG GGGGATGTGT	360
GT	362

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 475 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC GATATATGAA ACGTACAAA TATTATGAGT ATATAATATG	60
GGGAGACTTA ATCTAGTTTG GGGGATCAGG GCACATTTCT CTAAGAAAGT GACATTTGAA	120
TTGAGCTCTG AAGGATAAAT AGACATTACC CAGAAGAATA AAATGATGGG GAAGAAGGAG	180
GACATTTTCC GTAGATTTCC AGTGGCCCCN CTTGATCCCT TATCCACTCA TCACTNAGGA	240
GGATATTAAA TKCTATAGAA ATGGRAGRAA GACMMAAAGA GACCCTNATA TCTCGAGAGG	300
ATCCAGCMAA ATTCCAAGAG ACACAACAWT AAGAACTNG GAAGGAAGAG AAAAGGCMMN	360
NNAGGNAAAA GAAAGACAAG GAAATTNWN NAGNACGGAG AGAAAGAGAG AGGGAGCGTN	420
NAAGGGNACG AGAAAGGCGA GNACGGGGAC GAGAAAGGN AAGAGNACGT AAACG	475

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG	60
AAAAAGGACC GGAAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC	120
TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC	180
AGGGGACATA CCCCAATCTC TTGGTTCCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG	240
TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT	300
CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAAN TCCTAA	346

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAAACAGG GCTCCTGCTA GGAGATTGAN	60
ATTCTGGCTT TCCTTTGGAA CCCCTCACTG ACTCATCGCC CCTGAANCAG GANCCANCAG	120
GTNCCAAGGC TCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCCTG	180
GGCAGGCTGA RCCCANCCGA CTGGAACCAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG	240
GAAGGAGGCC AGATTCCTCC AGAACTGGGG RAGAGAACAG GTTTTGGGAAG TTGGGGGAGG	300
GTTTGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN	360
TTTTGNTANT CGTNCTTTGA ANACARNCCG CTTCCTTTCA ACCCTCCNCN TAAAAAGTTT	420
TGATNTTTTA AGG	433

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTTAT GNTAACTCTC ATGACAAACA CAATTTTAGT ACCTCTCACT	60
ACCAACTATC CAGGAACCAG GANTCACCTA TTA CTACGGT TCCAGCAGAA TGGGAATCCC	120
ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA	180
CCTCACCCCC TGA CTCTCC TCAANGGCTC TGCCAAGTCA AAAAAAAT CCTCTACATT	240

TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG	300
TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT	350

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA	60
TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA	120
CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN	180
CAATATGTGT CCTTTNACTN KGGKGTGAAC ATTTTTTYCTA TTATAAATYC TWAGAAAATA	240
TTNCTATGGN TATGAGATAT TKGATTCCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC	300
TGATGTKGGA NATTKGTTNC TAGTGTTYCA CTATTTAAAA AACAGNAAT ATCTGTCTNT	360
ATGCTNAGAG CTTNTYAGT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA	420
TTTTTGGGGC AAATTATCTA CATATTTATA ATTGTCTTGG TATTCCAAAT CTCGTTTTCC	480
AAAAGCTTAT ATCAATTTGT ACTTAACACC AG	512

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA	60
AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCAAGA GCTGNAGAAG CAGAGATAAG	120
NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA	180
CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTTCTNG AGGGGNAGAA AACAAAGGAA	240
GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGNAAAAT AAGTCCATAG GAGAATGTTG	300
NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AAACTGCCAA GAACCACTCA	360
TTCTCTAGA TACAMTTCCT GTAGGATCCY CCCAGACTTC CTCCCTTAAG CACGTCAGTA	420
TTCTCCTTAT TCTCCCTTCA TTTCAACCCT	450

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTCCTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC	60
ACTCACCCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGTAATA AAAGTCACCT	120
TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCTGTGT CCAGGAATAA CCTTTGNTAC	180
TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGA AAGGGACTTG GAAGCTCATA	240
GAATCCATGC CTCTTCTTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT	300
GTCTTCCCAA CTCAAACCCA TTTCTGAAG CCATTTCCCT GGTACTGNA TTGGCCACAA	360
CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTTT TAATGGCCTG CCAGTCTGGA	420
TTTGTCTTTG GCAACCAAC AATTTTGCTT CACAAGATTC CTACTTAAGG GAAGAGAGGG	480
GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG	540
AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTCNAGGTC CAACATCTCG	600
ACGTAAGGAG CGTTCCCAGT TCTTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC	660
ATCCCNAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT	720
GTTAACCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG	766

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNG GNGRARNGCC	60
CNTCGATCAC TTGGGANAGG NGA CTGTCMA TGTTTAATGA TTGTCANCCM NANAANTAAG	120
CTNACAGGGC AAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GRAKNAAATC	180
NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA	240
CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCCANTT TTTNNTTGNT	300
GANANACARC AATGCTGGCA TACNGTG	327

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATAACTNGTG TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA	60
AGAGNACGAG GGGGTAGCTG CCCCAATATA TTCTAATTTT TCTKGAGGAC CACCAAATNG	120
GMAGAGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAGGN ATCTTAGCCT CTAGGANAAA	180
AGAACCATTT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATTT ATNTCCAAAC	240
TCCTTATCCT GCCAATTCAG GGTCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA	300
TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG	360
TTKGGTNCTT TCCTTNCCTT NCCTTKGTTT AGCCTGTYCC GTCTACTNGG GGTGTCTTKG	420
ATTTGCTCCA G	431

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTTCCA CCAGACTTAC CAAATTTTAG ATGNATGGAA GAACTGTAAA TNCCATAAA	60
GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA	120
TGAAACTCTC AGCTGGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTTT	180
ATTATNTTTA TGGATGCCCC CTCAGAAAAA TATGNAANGG GGTAAGTAC TNGGAAATGG	240
GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT	276

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTTNCA CNAATAAAT TTACTGCTTT TTTYCTGTGA	60
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NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRNATGAG TYCAGTGGAT TATYCTNAGN	120
ACTAGAGTKG NKGTKGAAGN CATGGNACAT TTATATAGWT YWTTTCAGTTC TACACTAAAT	180
GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA	240
CATTGAGCAG TTGGATTACC AAGATCTCGA	270

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTTA GACTAGTTTC ATTATACTAC CAGTTTCTAA TATGTTGGTT TTTTATTCAC	60
TATTTGATAT ATTTGTTTTA ATATATGTTT TTGTTTTAGC AGGTAAAAGA ATCATAACAA	120
ATGTTTTTAA AAGAACATTA TTATTCTTTA ATAACGTCT TTTTATGCAT TTGGCATGCC	180
AACTTTTTTC ATTAACATCT TGGGTATTTT ATAAAAAGAG GGAAAGCTCA ATGTTTAACA	240
GGTAGCTTTT CTTAGGAGCT AAATTAAATA TTTAACAAAT CTCCTTCCCT TCNCCCTTCC	300
CCATCCCTCA AAGNATGGGT GNANTTATCT TTAACTTTGG GGCTNGCATC CNTGNAAGCT	360
TATGGNTANT CATAGTCTNA CMAAAGTAGG GTCACCNAAC TTGGCAGCAG AAATAATCTA	420
GTCTTACTGT GATAACTACC CAATTACTTT ATTATTTTTC CAGTTNCAGT TCCAAATGTT	480
TTGTGGNAAN AATTTTNNCT GTTTGTGATT TTCCAAGCTT AGAGGGGGAA ACCAACTTTC	540
CAGTGTGGA GAGCACTGNA TAGTTTATGN ATTGTGTAAA	580

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA NACAGAAAAA AATTTACTGA TNGGACATTG TTCTAAGTGT ATTATTGTAT	60
TAAATGGATC ATTTAATTTA ATCTTCATAA CTGACATAGG AGTTGAGTAA CTTGTGTGGT	120
CAAATAGCTA GTAAGTGATG AGTAGGCTGG GCGCAGTGGC TCAAGCCTGT AATCCCAGCA	180
CTCTGGGAGG CTGAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGNCA	240
ACATGGNAAA ACCTCGTCTC TACTAAAAAT ACAAAAATTA GCTGGGCGTG GTGGGNGCGC	300
ACTTGTAGNC CCAGNTACTC GGAAGGCTGA GGCAGGAGGA ATCGCTT	347

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 430 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCTCATCATG	CTTCACGGGG	GAGGCTGTGC	GGGAAGAATG	CTCCCACACA	GNATAAAGAA	60
TGCTCCCGCA	CAGGATAGAG	AATGCCCCCG	CACAGCATAG	AGAAGCCCCC	GCACAGCATA	120
GAGAATGCCC	CCNCACAGCA	TAGAGAAGCC	CCCGCACAGN	ATAGAGAATG	CTCTTCACCT	180
CTGGGTTTTT	AACCAGCCAA	ACTAAAATCA	CAGAGGGCAA	CACATCATTT	AAGATAGAAA	240
TTTCTGTATC	TTTTAATTC	TTTCAAAGTA	GTTTTACTTA	TTNCAGATT	CTATTTCTTT	300
ACTAGAATTA	AGGGATAAAA	TAACAATGTG	TGCATAATGA	ACCCTATGAA	ACAAACAAAA	360
GCTAGGTTTT	NTNCATAGGT	CTNCTCCNN	ATTGAATGAA	CGTCTNTCCT	CAAATTTANC	420
CCCCCAGGGA						430

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CAAACCCTAT	GNGAAATGGA	AAGGAACTA	TTCTAAAGCA	TAAAAGGTAG	AAATATATAT	60
ACCACCCATC	AAGAAAGATT	ATTTTTGNTG	AACTCAAGTC	ACCAGAGTGG	CTAAAGCCCA	120
GTAGAATGGA	AATGATTATA	TGGAAGGTGA	GGCCAACGGG	ACCAGAACAT	ACTGTGATAG	180
ACAGNAAGGA	GCTGTCTATC	TTCTATTCTC	CCACAGAAGG	AGGTGACTAA	GTCANCTGCC	240
CAAGCAATGT	TATATCTGCA	ATTGATGTNC	AGCAGTACAA	GTCTGAACAA	CTTGGATTGG	300
NTGATTAATG	TCCACANTAA	ACATACAAGT	CNTAATAGCT	ATCTCTATAT	AGTCTTTGGG	360
TNTTTACAAG	GCACTGNCAC	ATNATCTCAC	CTATTCCTCC			400

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 500 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA	ATTGAGTGNA	GNGTTCTCTG	GNCCACAGTC	TCGGTATCTN	CTGTGAAATG	60
GGGTATAGAT	TCTACAATAA	AACAAACACA	NNGGCCCTAG	GTCAGTGTTA	ATGGAGATCA	120
CCANCCACAT	TACCACCTCC	AACACAGAAT	TTTCTTTTTT	TTAATNCAAT	NCGTNTCTTA	180
TAAGTCACTT	TNCCCCAACT	CACCAATCTA	GNTAAGAATT	TTTACCCTGA	GAAAAACAGC	240
TACACTCTAA	AATTGCTNCA	AAGAAAATGT	CTAACATNTG	GAAAGAAGGA	CTTAACATGT	300
GANGNAGACA	CTGGCTCCAT	CTAGNGGGTG	CTTTNTTTTG	AAATAATTAT	AATNCCNCAT	360
CAAATTTTNG	GGGGNTACAG	CTTATTAGGA	ACTTGTTATA	GAACCAGATT	CTGCCACAGA	420
ANCCACGTGG	GTTGACAAGT	GGTTGNCAGA	AGAAAGGTAA	TATGGCTTAT	NATTAGGGNC	480
TCNCATCTGC	AGAGTAATTG					500

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG	ANNCAAATGT	CATCTAGTTC	CATCTCTACG	ACTCTCATGG	GGTCCAAAGA	60
AGAGTTTTAN	TTGAGTTTTA	GAATGTGAAG	TTGTGAAGTG	TCTGAAAAAC	TACATGGTGN	120
TCTGAAAGNC	AAACTTTTAG	CCTTGGGGGA	GAGCATCTAA	GACAGNAGGT	GAAGGGNAGG	180
GGTTAGAACT	AGAGGGATTG	AAGAATATTA	TCCATATAGG	TTAGGGTTAG	GTNNGGCAAC	240
GTTTTATAGA	ACAAACATTG	GCAAGCTACA	GCCACAGGCC	AGATCTGTCT	NCTACCTTCC	300
CACAAAGGTG	TAATAACAAA	GTTATTCACA	AATGTGTGAA	TAAACTNNCA	TTGGAAAGTG	360
CCCACGCTCC	TNGGTTTATA	CATTGTCTGT	GGCTGCTTTC	ACACTACAGT	AGCACAGGTG	420
AGTGTNTGCA	CTGGAGACCA	TATGCCCCAT	AGAGCTTTAA			460

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCAAGCAAC	AGTGTGTTAT	GCCTATACTC	CATGTTTATA	TGTGTGTATT	AAAAAATGTA	60
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TTTGTATATA TGTGTATGTA TAAGTGTGTG TGTGTGTATG ATGATTCTNC TCCCGNTTTG	120
AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA TACTGTCTGG	180
AAAAATGATT TATCTCCAC TTTGAAATTC CAAAATACGT ACATATATTT TTTTTTCTT	240
TTCTTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT AGTGTGATCA	300
TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCCCAG NCTCCTGAGT	360
AGNTGGGACT	370

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCCAT TCTGCTGGTG	60
GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAGTTAA TACAGAATTA	120
TTGGGTTGAT TTTCAACGTG TAGTTTAAGA TGAAGAGTTC CGNTTGGTTT AAACCACTTC	180
ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTTCGCAGT GTCANTGAAA ATCGTCCTGT	240
GACCACGCGT CAAGCTGCTG ATGGGGGACA GAACTTCCG GGNCTATCAT ATCTCCTTGA	300
NCTCGGCCCT CAAATCTGGT AGTTTCTGCA CCGAGGGACA CAGTCCACTG CGATGAAGTA	360
TGTTCAAAAT CGNTTCTTT AGGGAAGTCC TTCCAAAGTC CAATAGTGNA AGGTGGTCAA	420
GGAAGGATTT GGAAGGAAGN TGNAAAAGTC AGNCGGGAAT CTTGATTTGG NTAGNTGTGG	480
ANANAGGAAA TCACTTGGCC	500

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTCTTC CTTTGGNNG	60
GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC	105

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT	60
GTGTGAGCTA TGATCACACT ACTGCACTCC AGCCTGGGCA ACACAGCAAG ACCCTAAAC	120
TAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTTG GAATTTCAA GTGGGAGATA	180
AATCATTTTT CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT	240
CTTTCACCTT CAAAGCGGGA GAAGAATCAT CATAACACACA CACACACTTA TACATACACA	300
TATATACAAA ATACATTTTT TAATACACAC ATATAACAT GGAGTATAGG CATAACACAC	360
TGTTGCTTGA TAAATATAG GGATCC	386

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTTTATATG TGTGTATTAA	60
AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC	120
CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAAGCAT AAACCTTGGG TTTCAGATAC	180
TGTCTGGAAG AATGATTTAT CTCCCACTTT GAAATCCAA AATACGTACA TATATTTTTT	240
TTTTCTTTTC TTTTTTAGTT TNAGGGTCTT GCTGTGTTGC CCAGGCTGGA GTGCAGTAGT	300
GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTTCCT GCCCCAGNCT	360
CCTGAGTAGG TGGGACT	377

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 521 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT	60
CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG	120
AAGGGGTCAC ATATTAATCT CTGAAAATGG ATCTCTTGTT GGCTTTCATA CAAGGCAACA	180
GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN	240
G TTCAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT	300
CGGTTTTATT TTTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA	360
ATTTTGGNTT TTTAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA	420
AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG	480
CTAGGGAATA TTGNAAGAAN GTCCTCTCTA CAANAAANAA T	521

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT	60
GGGGTGCACT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC	120
TCCCACCTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC	180
TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAAGTC	240
TTGGGNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT	300
GAGCCACNTG CATCTGGCCT CAATTCACCT TTTAAATNCA AAATTAGGTT ACCTACTTTT	360
TATAAGGTAA TGTATTAGAA TTATTCTTNN NAAAAATAAA ACCGATTGTT GAAAGNGTGA	420
GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATACTC	480
CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC	516

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT TCTTAAAACA GAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
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TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGNTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GCGTGGTG	300
GTGCGCACTT GTAGTCCCAG CTA CTCTCGGAA GGGTTGAGGC AGGAGGAATC GCTTGGTCCC	360
CGGGAGGGAG AGGTTGNTNG TGNAGCTGAG ATCACGCCAC TNGCACTCCA GGCTGGGNAA	420
CAAAGGGAG ACCTTTNCTC AAAAAAAAAAT NAAAATAAAA AGTGATGAGT AGGATTGGGA	480
CCCNAGACAT CTTTCTCCA AGACC	505

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC AAACCCTTGT CCTGGGATCA AACAACTCTC CCACCTCAGC CTTCAAAGTA	60
GATAGAACTA CAGGCATGCA CTACCATGCC TAATTTTTTA AAAAAAATT TTTTTCAGA	120
GATGAGATCT CACTGTGTTT CCCAGGNTTG TCCGGAATC CTGGACTCAA GCGATCCTCC	180
CACCTTGGGC TGCCAAAGTG TTGGGATTAC AGGCATGAGC CACCATGCCT GGCCATACAC	240
TTTTTTTTTT TTTTAAANCA AGACGGAGTC TNGTTCTGTC GCCCAGACTG GAGTGCAGGG	300
GCGTNNATCT TGGCTCACTT GAAAGCTTCG CCTCCCAGGG TTCATGCCGT TCTCCTGNCT	360
CAGCCTCCCA AGTNGGTGGG ACTACAGGNA TCTGCACCAC GNCCGGTTAT TTNTTGGGTT	420
TGNNGNAGGG ACGGGGTTTC ACCATGTTAG GCAGGATGAC TTCGGACTTC CNGACCCAAG	480
ATCACCTGCTG TCGGCTCCCA	500

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA CGAGCCTGGG CAACACAGTG AGACTCTATC ACTACAAAAA AATTTTAAAA	60
TTAGCTAAAG TTGATGGNAC ATGCCTGCAG TCCCAGCTAC TCAGGAGGCT GGGGCAGGAA	120
GATAGCTTGA GCCTGGGAGT TAGAGGCTGT GTGAGCTATG ATCACA CTAC TGCACTCCAG	180

CCTGGGCAAC ACAGCAAGAC CCTAAACTA AAAAAGAAAA GAAAAAAAAA ATATATGTAC	240
GTNTTTGGGG AATTTCAAAG TGGGAGATAA ATCATTTTTC CAGACAGTNT CTTGAAACCC	300
AAAGTTTATG CTTAAATAAA GGTGTGCTTT CTTTCACCTT CAAANGCGGG AGAAGGATCA	360
TCATNCACAC ACACACACTN ATCATNCACA TTTTACAAA TNCAATTNNN NAATACAACA	420
CATTTTAACA TGGGGTTTTG	440

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 513 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT TCTTAAACA GAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGCTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GCGGTGGTGG	300
NTGCGCACTT GTAGTCCCAG CTACTCGGAA GGCTNGAGGC AGGAGGAATC GCTTGATCCC	360
NGGGAGGGAG AGGTTGGTNG TGANGCTGAG ATCACGNAC TTNACTCCA GNCTGGGNAA	420
CAAANGNGAG ATCTTNTCTC AAAAAAAAT AAAANTAAAA NGTGATGAGT AGGATTTGGA	480
CCCCAGACAT CCTNTCTCCA GGACCTGGNA TTC	513

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG	60
TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTAAATG ACTGCTAAAT CTCATTGTAT	120
GAAAATTTAT GTCCTAGCTA TAAAATTTGN TAGCACATGT TTAATTTTTT CTAATTTTCA	180
ATGTTTTTAAA CTAATATTTT CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTTT	240
NNTCCTCTTC GTACTCATTT TTATAGTTAT GGCCTGTGCA ACTGGTTTCC CATTTATATG	300

AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAGT AGTGAATTGT	360
CAACTTNGAG GGAAAAAAGT GAATTATTGG	390

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTC GTATATGGTA	60
AAACCCAAGA CTGATAATTT GTTTGTCA CA GGAATGCCCC ACTGGAGTGT TTTCTTTCCT	120
CATCTCTTTA TCTTGATT TA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA	180
ATCATTAAAT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT CGGCTGGGCA TGGTAGCTCA	240
TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG ATCACCTAAG CCCAGAGTTC	300
AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG	360
GGNATG	366

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGG	60
CCTTTCCAGT GAATGGAAAT CATTCCCACC ACACCAAAAT TCCAGATCAG GAGTGNAACA	120
GTAATGTAGT CCACAGCAAC GTTATAGGTT TTAAACACTT CCCTGAAAAA AAATTACACA	180
GATTTTAAAA GATGTACAAT AATTTCACC AAAACATTAT TTAGAATAAT GTGATGGCTC	240
CCAAACATTA GATATTAATN TCCCACCTTT ATAATTTTAC CATAACCTAT ATCAACTGTG	300
CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTTGTT TTTGTTTTTG	360
NGTTTGGAGC CAGTGTCTCA TTTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC	420
GGCTCAACTG NAGTCTTNC CTCNNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC	480
TAAGTTGGTT NGGANAAC	498

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAACAG GGNCATGAGG GCACTAATCA TAATGAGATA TGCCTGCTGG AGTCGAAGTG	60
GACCTTTCCA GTGAATGGAA ATCATTTCCCA CCACACCAAA ATTCCAGATC AGGAGTGAAA	120
CAGTAATGTA GTCCACAGCA ACGTTATAGG TTTTAAACAC TTCCCTGAAA AAAAATTACA	180
CAGATTTTAA AAGATGTACA ATAATTTCCA CAAAACATT ATTTAGAATA ATGTGATGGC	240
TCCCAAACAT TAGATATTAA TNTCCACCT TTATAATTTT ACCATAACCT ATATCAACTG	300
TGCTATTATT TATTTAATNC TTCCCTCTAA ATTAATTTAC TCTTTTTTTG TTTTGTGTTT	360
TGTGTTTGGA GCCAGTGTCT CATTTTGGTT GCCCAGGCTT GGAGTAAAGT GGGTGCAATC	420
ACGGCTCAAC TGNAGTCTTT ACCTCCCGGA GATCANGTTG GTCTTTCCC	469

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 370 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTTATCAAG TACCTCCCTG AATGGACTGN GTGGCTCATC TTGGCTGTGA TTTCAGTATA	60
TGGTAAAACC CAAGACTGAT AATTTGTTTG TCACAGGAAT GCCCCTGAGG AGTGTTTTCT	120
TTCCTCATCT CTTTATCTTG ATTTAGAGAA AATGGTAACG TGTACATCCC ATAACTCTTC	180
AGTAAATCAT TAATTAGCTA TAGTAACTTT TTCATTTGAA GATTTCCGGCT GGGCATGGTA	240
GCTCATGCCT GTAATCTTAG CACTTTGGGA GGCTGAGGCG GGCAGATCAC CTAAGCCCAG	300
AGTTCAAGAC CAGCCTGGGC AACATGGCAA AACCTCGTAT CTACAGAAAA TACAAAATT	360
AGCCNGGNAT	370

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 316 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCATGGTGT TGGCGGGGAG TGTCTTTTAG CATGCTAATG TATTATAATT AGCGTATAGT	60
GAGCAGTGAG GATAACCAGA GGTCACTCTC CTCACCATCT TGGTTTTGGT GGGTTTTGGC	120
CAGCTTCTTT ATTGCAACCA GTTTTATCAG CAAGATCTTT ATGAGCTGTA TCTTGTGCTG	180
ACTTCCTATC TCATCCCGNA ACTAAGAGTA CCTAACCTCC TGNAAATTGA AGNCCAGNAG	240
GTCTTGCCCT TATTTNACCC AGCCCCTATT CAAAATAGAG TNGTTCTTGG NCCAAACGCC	300
CCTGACACAA GGATTT	316

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGCAGNCCG GGGGATCCTG GTAAAGTCA CAAGGTCAGC CTACTAAAGC AGGGAAAAC	60
AAAGGCAAGT AAACACGTGC AGACAAAAA AGGGATAAAG AAAAGGAATT AAGAACTAG	120
CATTTTAAAN GTGGGGGAGG TGAATGCTTC CCAGAATGGG TTTATATCAC TTGCTTGNGG	180
GCCTTCTGAG TGTTGGNAAC AACCTGTCAT CATCACACAT ACCTGTCATC TTTAATGGTC	240
TCCATACATT ACTAATAGAT TATACAGATG GCCATCACTT AACACTTCCA CTCACTCAAT	300
TTGTNCAACA TGCAAGGTTA CCCTCTTTTT TNGCTTACNG CCACAAAGCA TTGGANAAGG	360
TTTGTGATTT TTAGTAGCCN CCACTTCATC AAATTTAAGC ATTTTCTTTT TCCTNTTAAC	420
ANCCAGGACA GGNTTNAACN AAGGAAAT	448

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTTT TTCAAATTCA GCTTTCTGTG ATTCAGACC ACATATGCAA	60
GGAACATCT TACCTTAATT AATAAGACTT TAAATCCTT GTGTCAGAGG CGTTTGGACC	120
AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAATAAGG CCAAGACCTA CTGGGCTGCA	180
TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA	240



GCTCATAAAG GATCTTGCTG ATAAACTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC	300
AAAACCAAGA TGGTGAGGAG AGTGACCTCT GGTTATCCTC ACTGNTCACT ATACGNTAAT	360
TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT	420
NCCATGGNAA CGNNCCCGGA NGNTANCTTG	450

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 388 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG	60
GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTTATA TTTTAGTAG AGACGGGGTT	120
TCACCATGTT GGGCAGGCTG GTCTCAAACCT CCTGACCTCA AGTGATCTGC CCACCTTGGC	180
CTCCCAAAGT GCTGGGATTT CAGGCGCCTG GCCTGTTACT TGATTATATG CTAACAAGG	240
GGTGGATTAT TCATGAGTTT TCTGGGAAAG AGGTGGGCAA TTCCCGGAAC TGAGGGATCC	300
CTCCCCTTNN NAGACCATAC AAGGTAACCT CCGGACGTTG GCATGGNATC TTGTTAAACT	360
TGTCATGGNG TTGGGGGGGA GTGTCTTT	388

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAGT ATGTTTCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA	60
ACACATAAAT TCTTTTCCAC CTCAGGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT	120
ATTCTTTCCT TTTCTAACTT TGGTGGATTA AATTCCTGTC ATCCCCCTCC TCTTGGTGTT	180
ATATATAAAG TNNTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTTAA	240
TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGCAC CCNTACAGAT GGAACAATGG	300
CAAGCGCACA TTTGGGACAA GGGAGGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC	360
NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTTAA ACTAATTCCA	420
ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTTGG GAGGAGTCAA GGAAGAGNAG	480

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT	60
GTTTCTCATT CACAGAAAAA CATTTTATT CCAGGTGCCA ATATTCCCAG CAAAAAGAC	120
TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC	180
TAGGGAGATG TGTTGTGTAT GGAACCTCTA AGGAGAGAAT TCTGCTGACA TGTCTATGT	240
TCTTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC	300
CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA	360
ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA	420
GTATGTGCAT TATTT	435

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 439 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT	60
CAGCTTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA	120
AAGCCAGTGT GGCTTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA	180
GGGGCATGAC TTAGCTGGAG AGCCCATCCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG	240
AGGGGTTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAAGT ATGTTTCCTG	300
TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAT TCTTTTCCAC	360
CTCAGGGGCA TTGGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTTCCT TTNCTNACTT	420
GGGNGGATTA AATTCCTGT	439

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGGTCCAAA GAAGAGTTTT AATTGAGTTT TAGAATGTGN	60
AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCAAACTTTT AGCCTTGGGG	120
GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT	180
TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTTATA GAACAAACAT TGGNAAGCTA	240
CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA	300
CAAATGTGTG AATAAACT	318

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 450 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTCNTTTTT TTTTTTNTT TTTTTTNNTT TTNGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGA ACTCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA GCCGTGATTG CANCCACTTT ACTCCNAGCC TGGGCAANCA AAATGAGACA	60
CTGGCTNCAA ACACAAAAAC AAAACA AAAAGAGTAAA TTAATTTAAA GGGAAGTATT	120
AAATAAATAA TAGCACAGTT GATATAGGTT ATGGTAAAAT TATAAAGGTG GGATATTAAT	180
ATCTAATGTT TGGGAGCCAT CACATTATTC TAAATAATGT TTTGGTGGAA ATTATTGTAC	240
ATCTTTTAAA ATCTGTGTAA TTTTTTTTCA GGGAAGTGTT TAAAACCTAT AACGTTGCTG	300
TGGACTACAT TACTGTTGCA CTCCTGATCT GGAATTTTGG TGTGGTGGGA ATGATTTCCTA	360
TTCCTGGAA AGGTCCACTT CGACTCCAGC AGGCATATCT CATTATGATT AGTGCCCTCA	420
TGGCCCTGGT GTTTATCAAG TACCNCCTG AATGGACTGG GTGGCTCATC TTGGCTGTGA	480
TTTCAGTAT	489

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCGGCT AATTTTTGTG TTTTCTGTAG ATACGAGGTT	120
TTGCCATGTT GCCCAGGCTG GTCTTGAAC CTGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCTGTGA	360
CAAACAAATT ATCAGTCTTG GGTTTTACNA TATACTGAAA TCACAGCCAA GATGAGCCAC	420
GCAGTCCATT CAGGGAGGTA CTTGATAAA	449

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT TCCCGACCCG AGCCTGGTGC CCCTTCCCCA TTATGATCCT TNTCGCTTCC	60
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GGCGGCATCG GGATGCCCCG CGTTGCAGGC CATNCTGTCC CAGNCAGGTA GATGACGACC	120
ATCAGGGACA GCTTCAAGGA TCGCTCGCGG CTCTTACCAG CCTAACTTCG ATCATTGGAC	180
CGCTGATCGT CACGGCGATT TATCCCGCCT CGGCGAGCAC ATGGAACGGG TTGGCATGGA	240
TTGTAGGCGC CGCCCTATAC CTTGTCTGCC TCCCCCGCGT TCGCTCGCGG TGCATGGAGC	300
CGGNCCACCT CGACCTGAAT GGAANCCGGC GGCACCTCGC TAACGGATTC ACCACTCCAA	360
GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC NCAAAACCAAC CCTTGGCAGA	420
ACATATCCAT CGCGTCCGCC ATCTCCANCA GCCGCACGCG GCGCATCTCG GGCAGCGTTG	480
GGTCCTGCAG	490

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 470 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGTT TAAAAAATAA AATAAACTAA AAGTTTATTT ATGAGGAGTA CACTGCTTTC	60
TTGTAAACAC ATGTACAAGC CATATAATAG AGTTCATTTT NNACCCTAGT TACGGAAACA	120
CTAGAAAGTC TNCACCCGGC CAAGATAACA CATCTTTAGG TAAAAATAGC AAGAAATATT	180
TTATGGGTTG TTTACTTAAA TCATAGTTTT CAGGTTGGGC ACAGTGGNTC ATGCCTGTAA	240
TCCCAGCACT TTATGCGGCT GAGGCAGGCA GATCAGTTGA GGTGAGAAGT TTGAGACCAG	300
CCTGGGCAAT GTGGCAAAAC CTCATCTCCA CTAAAAATAC AAAAATTAGC CAGGCATGGT	360
GGTGACACA TGTTAATTCC CAGCTACTTG GGAGGNTTGA GACAGGAGGG TCGCTTGGNC	420
CTAGGAGGGA AGAAGTTGNA GGGANCTTAA TGTCACTGCA CTCTAGNTTG	470

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 445 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATTC TGAATGCTGC CATCATGATC AGTGTCATTG TTGTCATGAC TANNCTCCTG	60
GTGGTTCTGT ATAAATACAG GTGCTATAAG GTGAGCATGA GACACAGATC TTTGNTTTC	120
ACCCTGTTCT TCTTATGGTT GGGTATTCTT GTCACAGTAA CTTAACTGAT CTAGGAAAGA	180

AAAAATGTTT TGTCTTCTAG AGATAAGTTA ATTTTtagTT TTCTTCCTCC TCACTGTGGA	240
ACATTCAAAA AATACAAAAA GGAAGCCAGG TGCATGTGTA ATGCCAGGCT CAGAGGCTGA	300
GGCAGGAGGA TCGCTTGGGC CCAGGAGTTC ACAAGCAGCT TGGGCAACGT AGCAAGACCC	360
TGCCTCTATT AAAGAAAACA AAAACAAAT ATTGGAAGTA TTTTATATGC ATGGAATCTA	420
TATGTCATGA AAAAATTAGT GTAAA	445

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTTA TACTGAACCA CCAGGAGGAT AGTCATGACT ACAATGACNC TGATCATGAT	60
GGCAGCATTG AGAATTGAGT GCAGGGCTCT CTGGCCCACA GTCTCGGTAT CTTCTGTGAA	120
TGGGGTATAG ATTCTACAAT AAAACAAACA CAAAAGCCCT AGGTCAGTGT TAATGGAGAT	180
CACCAACCAC ATTACCACCT CCAACACAGA ATTTTCTTTT TCTTAATTCA ATTCGNATCT	240
TATAAGTCAC TTTTCCCCAA CTCACCAATN CTAGCTAAGA ATTTTTAACC TGAGAAAAAC	300
AGCTACACTC TAAAAATTGCT TCAAAGAAAA TGTCTAACAT ATGGAAAGAA GGACTTAACA	360
TGTGAAGCAG ACACTGGCTC CATCTAGTGG GTGCTTTATA TTGAAATAAT TATAATACCT	420
CATCAAATTT TTTNGGGTAC AGNTTATTAG GAACTTGGTA TGGAAACCAGA TTCTGCCACA	480
GAAACCACGN GGGCTG	496

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC	60
TATTGTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAATC	120
AAGGTAACGG TTAGACCTGG GATTAACAAC AGACCCGTCA CTATGAGTTC TAAAAACCTG	180
AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTTAAA AGTCTAGATT ATCTATCATT	240
GTTCACTGAA GGCATTGAGG TCCTCTCTTT TACCTGGGTC TTGGNTTGCT CCATTCTCTC	300

TGTTTCATCCC AACATACACA ATTGTACTTA TCCTTTGAGA TGTACCTTAA ATACTGACAC	360
CTGCATGAAA ACTTGTTTAC TGGCTGCAGG TCCAAGCACC TTTTTCNAAA TTCAGCTTTC	420
TGTGATTTC AACCACATAT GCAAGGAAGT ATCTTACCTT AATTAATAAG ANTTTAAAAAT	480
CCTTGTGTCA GAGGCG	496

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 368 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGANCGCTT GGGCCCAGGA GTTCACAAGC AGCTTGGGCA ACGTAGCAAG ACCCTGCCTC	60
TATTAAAGAA AACAAAAAAC AAATATTGGA AGTATTTTAT ATGCATGGAA TCTATATGTC	120
ATGAAAAAAT TAGTGTAATA TATATATATT ATGATTAGNT ATCAAGATTT AGTGATAATT	180
TATGTTATNN NGGGATTTC AATGCCTTTT AGGCCATTGT CTCAAAAAAT AAAAGCAGAA	240
AACAAAAAAA GTTGTAACGT AAAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG	300
TTTTTGNTTG TTTGTTTGNT TGTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG	360
AAGTGCAG	368

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCTTT TTTTTTTTTT TTTTTTTTTT TTNCTCCTAA TGTTTTTATT GTNCCTTAGA	60
TAAGTGGATA GNACAAAGT NGNCTTNGTT TTTTACTTAA AAAACGTACT TTCCGCATAC	120
TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCCAGG TGAGCCCTTC	180
CTATCTGNGG NTACATGATT TAGCTAATTT AACAGAAGA GAGTAATTCC TTNGGATTAT	240
TATCAACATG AAAGTTGGAC TATGTCTCTA TAAGGGTGAA CACTGATTTT TTTTTCTTT	300
TTAGAAACAA AAACCATCCA CTTATTAATC CAACTACGG GATTGGATTT ACAACAATCA	360
TCGCATNAAC TGAACATACG AAGTTACCAC TCAAGGGAAT NACAGAAGAA CGTTGNACAA	420
TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACTTCA NTCTACAAAN	480
TCTGACCATC GNTTCAGTAT	500

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCTTT ACTCTTCTTT AATTCTACCG TCTTTGGGCA TACATCTCAT TTGNTGTGGA	60
AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCATAAC ACATTCTTTT CATCATACAA	120
AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT	180
GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGGCAA	240
GTGAGCGTAC AAGTATNTCT ACAAATTCAG AATTTGGTGG AAAATCCAAA TTTGNCTTCA	300
ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTTAC TGAATTTGGG	360
AACCTGAGGT TAAAACTTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNNGGAAG	420
GAATGGAAAC ACAGACGGGA ATGAGTNTCA	450

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAAACTAGGA	60
ATAGCCCCCT TTTACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC	120
CTGCTTCTTC TCACATGANA AAAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC	180
CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCGGG	240
TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG	300
ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG	360
GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAGTT CCAGAGCCAC ATCATCATCA	420
GGTTTGGACC TGAAGANAGA GAACATCCTC	450



(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 500 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTT TAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTT TA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGTAACTAAG AGTACCTAAC CTCCTGCAAA TNGCAGCCCA	300
GTAGGTCTTG GNCTTATTTT ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA	360
CGCCTCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA	480
ACAAGTTTTT ATGCAGGTGT	500

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 500 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC	60
CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA	120
ATGTTTATTT TTCAGTTACA ACTTTTTTTT TTTTCTGCTT TTATTTGTTG AGACAATGGC	180
CTAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAATAATC	240
ATAATATATA TATTTTACAC TAATTTTTTTC ATGACATATA GATTCCATGC ATATAAAATA	300
CTTCCAATAT TTGTTTTTTT TTTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTTGCCCAAG	360
CTGCTTGTGA ACTCCTGGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATT	420
CACATGCACC TGGCTTCCTT TTTGTNTTTT TTGAATGTTT CACAGTGAGG AGGAAGAAAA	480
CTNAAAATTA ACTTATCTCT	500

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACTTGTCA	60
GCCCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC	120
AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATATAA GCACCCACTA GATGGAGCCA	180
GTGTCTGCTT CACATGTTAA GTCCTTCTTT CCATATGTTA GACATTTTCT TTGAAGCAAT	240
TTTAGAGTGT AGCTGTTTTT CTCAGGTAA AAATCTTAG CTAGGATTGG TGAGTTGGGG	300
AAAAGTGACT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATCTGTG TTGGAGGTGG	360
TAATGTGGGT GGTGATCTC ATTAACACTG ANCTAGGGNT TTGGGGTTTG GTTTATTGTA	420
GAATCTATAC CCCATTCANA GAAGATACCG	450

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT	60
AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTAA	120
AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA	180
TACTTCCTGT ACATTGTTTT TTCTTGCTTC AGGTTTTTAG AACTCATAGT GACGGGTCTG	240
TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAAT	300
GTTTTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG	360
CCTTGGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACCTCCG GCAGGTGGTG	420
GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC	480
ATGCTCNTTG GCCCTGTGAN TC	502

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCAGTGT	CCTTTTCTCC	ACTTAAACA	TGAAGTAATA	ACCCCTCGNT	CTCTCAACTG	60
CTCCTGACCA	TCACAGAGGA	TGGGCTCTCC	AGCTAAGTCA	TGCCCCTTCA	ATGNAGAGGC	120
CTTCAAGGTG	ATGATGACAT	GCTGTAAAGA	AAAGCCACAC	TGGGTTTGAG	AATAATAAAA	180
CAAACTCAT	ACGTACAGCT	GCCCATCCTT	CCGGGTATAA	AAGCTGACTG	ACTTAATGGT	240
AGCCACGACC	ACCACCATGC	AGAGAGTCAC	AGGGACAAAG	AGCATGATCA	CATGCTTGGC	300
GNCATATTTT	AATGTCAGNT	CCTCATCTTC	TTCCTCATCT	TGNTCCACCA	CCTGCCGGGA	360
GTTACCNTGG	GTCGTCCATT	AGATAATGGG	TCAGGGTGGC	CAAGGCTCCG	TCTGTCGTTG	420
TGCTCCTGCC	GTTCTCTATT	GTCAATCTAT	AAGCACAAGA	AAAACATTTN	CAGTAAATCA	480
GATNCTCAGC	AGAATCAAG					499

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAACTCCCAG	GNTCAAGATN	TCTNCCTGCG	TTAGCCTCCT	GAGTAGCTGG	GACTATAGGT	60
ATGTGCCACT	ATTCTGAAA	ACATAATCAG	TTTTGAAGGT	AGTGTCTGGG	CTGGGCGCAG	120
TGGNTCACGC	CTTCAATCCC	AGCACTTTGG	GAGGNCGAGG	TGGGCGGATC	ACCTGAGGTC	180
AGGAGTTCGA	GACCAGCCTG	ACCAACATGG	GATAAGACTC	CATCTCTACT	AAAAATACAA	240
AAAATTAGCC	AGGCATGGTG	GNGCATGCCT	GTAATCCCAG	CTACTCAGGA	GGNTGAGGNA	300
GGAGAATTGG	TTGGAACCTA	GGAAGCAGAG	GCTGTGGTGG	AGCCGAGATC	GCACCATTGG	360
ACTCCAGGCT	GGGNAACAAG	AGTGAAAATC	CNTCTTAAAA	AAAAAAAAAA	AAAGGTAGNG	420
TTTGNCCGG	NGCGGGGGGT	CACGCCTGTA	ATCCCAGNAT	TGGGGANGGC	AAGNGGGGGG	480
GTCANNANGN	NAGNAGTCCG					500

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT GACATGTCCT ATGTTCTTTT CTCCCCTACT CCTTCCTACT GTCAGNAATG	60
AAGGGTAGGG CTCCAGCCTG GACCCTGAAG TAAGCTAGAG GTTAGAAGCT AAAGAAGAAA	120
GAAGGAGATT GAGTCCTTNG ATGAACGTGA AGCCACCGTA CTAATCTGGA CTGCCTACCT	180
CTGCACTACT CTATGAGAGA GAAAGTATGT GCATTATTTA AACCAGTTGG GTTGATTTTC	240
TATTAACAAA GTCAGAAACA TCTCTGTAAA AAGCCAGACT GAATATTTTA AGCTCTATGG	300
GTCATATGGT CTCCAGGGCA AACACTCAAC TGTGCTACTG TAGTGTGAAA GCAGGCACAG	360
ACAATGTATT AACCAAGGAG GGTGGTCACT TTCCAATGAA AGTTTATCAC AAATTGGNGA	420
ATACTTGGTA TTACACCNNG GGGGAAGGTA GGAGAAGATC TTGCCTGTGG TTGTNGNTGG	480
CAATGTTGGT CTTTTATACG NG	502

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 495 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC CTTAGAAGTT CCATACACAA CACATCTCCC TAGAAGTCAT TGCCCTTACT	60
TGTTCTCATA GCCATCCTAA ATATAAGGGA GTCAGAAGTA AAGTCTGGNT GGCTGGGAAT	120
ATTGGCACCT GGAATAAAAA TGTTTTTCTG TGAATGAGAA ACAAGGGGAA GATGGATATG	180
TGACATTATC TTAAGACAAC TCCAGTTGCA ATTACTCTGC AGATGAGAGG CACTAATTAT	240
AAGCCATATT ACCTTTCTTC TGACAACCAC TTGTCAGCCC ACGTGGTTTC TGTGGCAGAA	300
TCTGGTTCTA TAACAAGTTC CTAATAAGCT GTAGCCAAAA AAATTTGATG AGGTATTATA	360
ATTATTTCAA TATAAAGCAC CCACTAGATG GAGCCAGTGT CTGCTTCACA TGTTAAGTCC	420
TTCTTTCCAT ATGTTAGACA TTTCTTTGAA GCAATTTTAG AGTGTAGCTG TTTCTCAGGT	480
TAAAATTCTT AGTAG	495

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 500 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTTGTC ACAGTAACTN AACTGATCTA GGAAAGAAAA AATGTTTTGT	60
CTTCTAGAGA TAAGTTAATT TTTAGTTTTTTC TTCCTCCTCA CTGTGGAACA TTCAAAAAAT	120
ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG	180
CTTGGGCCCCA GGAGTTCACA AGCAGCTTGG GCAACGTAGC AAGACCCTGC CTCTATTAAA	240
GAAAACAAAA AACAAATATT GGAAGTATTT TATATGCATG GAATCTATAT GTCATGAAAA	300
AATTAGTGTA AAATATATAT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA	360
TTTTGGGATT TCAATGCCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA	420
AAAAAGTTGT AACTTGAAAA ATAAACATTT CCATATTTAT AGCCAACTAA GTGGGTTTNG	480
GGTNGGTTGG GTTGGTTGGT	500

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTA A CAGGTCCAC AACCCCTAAA AAGTACAGAT TTTTTTTTTC TTNGTGGAGA	60
CAGGGTCTCA CTTGGTCGCC CAGACTGGAG TGCAGTGGCA CGATCTCAGT TCACCACAAC	120
CTCTGCCTCC TGGGTTCAAG CAATNCTCGT GCTTAAGCCT CCTGAGTAGG TGAACCACG	180
CGTGCGCGCC ACCACGCTAG GTTNATTGTG GCTTTTTTTAG TAGAGACAGG GTTTCGCCAT	240
GTTGCCCAGG CTGGTCTCAN ATTCCNGACC TCAAGTGATC CGNCCGCCTC AGACTCCCAA	300
AGTGNTGAGC ATTACAGNTG TGTACCACTA TGTCCCNGNC CNCATCTCTC TTTAAAACAN	360
CTTNCATTTA CCTAGTCCAC TCCTG	385

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA AGAAAGCATT TCAANNTAAT TAACAGGTCC CACAACCCTT AAAAAGTACA	60
GATTTTTTTTT TTCTTTNNGG AGACAGGGTC TCACTTTGTC GCCCAGACTG GAGTGCAGTG	120
GCACGATCTC AGCTCACCAC ANCCTCTGCC TCCTGGGTTC AAGNANTTCT CGTGCTTANG	180
CCTCCTGAGT AGGTGGAACC ACGCGTGTGC GCCACCACGC TAGGCTACTT TNTGTATTTT	240
TAGTAGAGAC AGGGTTTCGC CATNTTGCCC AGGCTGNTCT CAAATTCCTG ACCCNCAAGT	300
GATCCCCCN CCTTCAGTAC TCCCCATCAG	330

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGNCGTT CTAGAACTAG TGGCNCCCAA GGNAGAAGAA GTTTTCTTAG TACAGAACAA	60
AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTTCT	120
CANTCTTTCC NCCACCTTTC CCGTCTTTCT ATTCCACAAA GCCGNCATTG TCATCCTGGC	180
CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGGG	240
TCCTCACTTC CCAGTAGGGG TGGCCGNGCA GGNGGTGCCC CNCACCCCCC GGGCGGGGTG	300
GTTNGTCCNN CCGGNGGGNT GCACCNCCCC CACCCTCCC CNCTCTNCTA CTGGCGGTG	360
TNTATTNCAN NATCTTTAAG CA	382

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTACTGNTCA GTGCCCACCC	60
GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC	120
TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG	180
GNATCTCTGC TTCACCAGTG TCCAGGGGTT GCACAATTCT TGTTTACTCG TAGGATATTT	240
AATCTTGGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT	300

GTATTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTTN GTGGNAATGG AGTTTCACTC 360

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCTTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT	60
GAGAGTGTTA CAGTCTAATT CTATATCACA TGTAACCTTT ATTTGGATAT ATCAGTAATA	120
GTGCTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT	180
CGCCAGGTTG GAGTGNAATG GTGCGATC	208

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 470 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGGCGTC GATATTTGTT GCGGAATACT	60
CCCCTGACCG TAAACGTGGC TTTATGGGCA GCTGGCTGGA CTTCGGTTCT ATTGCCGGGT	120
TTGTGCTGGG TGCGGGCGTG GTGGTGTTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC	180
TCGATTGGGG CTGGCGTATT CCGTTCTTTA TCGCTCTGCC GTTAGGGATT ATCGGGCTTT	240
ACCTGCGCCA TGCGCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AAACTGGAAC	300
AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTTAAAGAG ATTGGCACTA	360
AATACTGGNG CAGNCTGTTG AATGTTTGGG CTTGGTAATT GGCAACCAAC GTGATTACTA	420
NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC	470

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 440 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT	60
ATTGNTGNTG CTCTTTTTTA CATNCATTTA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG	120
TCTTTCAGAA TTAACACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT	180
GATGAATTAC TCTGAAGTTT TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAG	240
ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA	300
CTGAAAGNAA CTTAAGACTA CAGTTAATTC TAAGCCTTTG GGAAGGATT ATATAGCCTT	360
CTAGTAGGAA GTCTTGTGCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT	420
AAANACCAAA AATAATTGAT	440

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAA CAGAACTTTG TGCACTACAA	60
TTATACTGTT ATAAAAACA CTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC	120
ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAA GGCTGTTGTC ACTTGCAGGC	180
TCCCAGATTA GGTCTGAAAT AGGATTTTAC CAGGTCATCC ATTGTTAGTT AAATCCTAGT	240
AAATTCATTT ANACCAATCA AATACTTATA AGACCAATTT GTAAACCAGG AATGTATTAA	300
TTTGTACGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAAGGTAG GACTCTTTAG	360
CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTTCAA CCCACAAANG ATACTTTAAT	420
GACTTTCTGA TTTNCCAGCA AAAGGGGGG	449

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG	60
GCTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT	120
GCAGTGGTGC AATCTTGGTT CACTGNAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGC TAAATTTGGN	240



ATTTTTTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTCCTGA	300
CCTTGTGATC CACCAGCCTC GGCCTCCCAA ATGNTGGGA TTACAGGCGT GAGCCACCAC	360
AACCAGGCTA AAGTTTTAA ACATGCCAAG TGTATTACA TAATGCGATA CGANTTATGT	420
ACATA	425

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNTTGTA AATAAGCATG TTATCTGTCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCTCCCTTTG GTGTATATCA GNNGTCANNA	360
CNTATCTTNG GGGCTGAAAA ATGTTT	386

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 224 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA AGAAAAACAG AACTTTGTGC ACTACAATTA TACTGTTATA AAAAACAATT	60
CCATAGATTA CATTAAGCAG AAACAAACCT TTCTTTCATG TGTTCCTCCTC CAGGCCAAGC	120
TGTCTAAGGA CCGCAAAGGC TGTGTCACT TGCAGGCTCC CAGATTAGGT CTGAAATAGG	180
ATTTACCAG GTCATCCATT GTTAGTTAAA TCCTAGTAAA TNCA	224

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 440 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCC	TCCTCGGC	CTCCAAAG	TGT TGGG	ATTACA	GGCGTG	AGCC	ACCGCACCTG	60
GCTTTTTT	TTTTTTTT	TGGNGG	AGAC	AGAGTCTT	AC	TCTGTTG	CCC AAGCTGGAGT	120
GCAGTGGT	GC AATCTT	GGTT CACTG	CAACC	TCCACCT	CCA	GAGTTCA	AGC AATTCTCTGC	180
CTCAGTTT	CT GGAGT	AGCTG	GGATTAC	AGG	TGCCTG	CCAT	CACGCCTGGN TAAATTTGGG	240
ATTTTTTT	TTT AGTAG	AGACA	GGGTTT	CANC	ATGTTG	GCCA	GGNTGGTCTT GGA	300
CCTGGTGA	AC CACCAG	GCTC	GGGCTC	CAAA	TTTGGT	TGGG	ATTACAGGGG GTNAANCAAC	360
CACAACCC	AG NCTAA	AGTTT	TNAAA	CATN	CAAAGT	GTTT	TAAATNATG NGATACGATT	420
TATTGTAC	AA TTAAT	TTTAT						440

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTTCCA	TCTTCTCC	AGAGTTT	GTG CCTT	ACATTA	TTACTC	CTTG	CCATTTTCAA	60
GAAAGCAT	TG TCAGCT	CTTC	CAATCT	CCAT	CACCTT	TGGG	CTTGTTTTCT ACTTTGCCAC	120
AGATTATC	TT GTACAG	CCTT	TTATGG	ACCA	ATTAGC	ATTC	CATCAATTTT ATATCTAGCA	180
TATTTGCG	GN TAGAAT	CCCA	TGGATG	TTTC	TTCTTT	GA	CTGATAAATA CTGGGGAGGA	240
CAAAGGTG	AT TTTCTG	TGT	CCACAT	CTAA	CAAAGT	CAAG	ATCCCCGGCT GGACTTTTGG	300
AGGTTCC	TTT CAAGT	CTTCC	TGACCAC	CTT	GCACTAT	TGG	ACTTTGGNAA GGAGGTGCCT	360
ATAGAAA	ACG ATTTT	GGAAC	ATACTT	CATC	GCAGGG	GGAC	TGTGTCCCCC GGTGGCAGAA	420
NCTACCA	AGA TTTG	CGGGNC	GAGGT	CAA				448

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCC	GCCTTG	GCCT	CCCAAAG	TGC	TGGG	ATTACA	GGCATG	AGCC	ACCGCTCCTG	60
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GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTTNAGTAA AATAAGNATG TTATCTGNCC GCCCTGCCTN	180
GGNNATTGNG ATAAGGAT	198

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG CCGTGATTGC ACCACTTTAC TCCAGCCTGG GCAACAAAAT GAGACCCTGG	60
CTCAAAAACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTAAAGGGAA GTATTAAATA	120
AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGATA TTAATATCTA	180
ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTNTTGG TGAAAATTAT TGTACATCTT	240
TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT TGCTGTGGAC	300
TACATTACTG TTGCACTCCT GATCTGGAAT TTTGGGTGTG GTGGGAATGA TTTCCATTCA	360
CTGGAAAGGT CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCTCATGGNC	420
CTGGTGTTTA TCAAAGTACC TCCCTGAATG GACTGCGTGG GTCATCTTGG NTGTGATTCA	480
GTATATGGTA AAACCCAAGA	500

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCGGCT AATNGNTGTA TTTTCTGTAG ATACGAGGTN	120
TNGCCATGTT GCCCAGGCTG GTCTTGAAC CTGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTNA	360
CAAAACAAAT TATCAGTCTT GGGGTTTAC CATATACTGA AATCACAGGC AAGATGAGCC	420

ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG	480
AGATATGCTG CTGGAGTCGA	500

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCCTGCGCT ACGCGCTGCG GCGGACCAAA	60
TTCTTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCCCT TTTTAAAATT	120
AATTTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG	180
CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCCGCAT GGAACCCATA AAACCTTAAG	240
CAATGGTACG TTGGATCTCG ATGATTTCGA ATACTTCGAT CACATCGNCA GTGCGGACGT	300
CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA	360
TCTTTGGAAG CGGGGCAGGG ACTCCAGCTC GNCTTCGTAG ATAACCACGT TGGCACGCAG	420
GAACGCGGGT CGGGTTGTGA CGTTTAACAC AACTTCCGGG TAACCATACA GGCTGNGATG	480
GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT	540
TGTTCA GTTC	550

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 541 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA	120
TNTTGT TTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC	240
CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG	360
AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTTACTCC TGTAAGTATT	420

TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTTAT CGGGAACCTG AAGANATGTN	480
ACTATGGCAA TTTCANGGNA CTTGTCTCAT CTAAATGAN AGNATCCCTG GACTCCTGNA	540
G	541

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCNCNCN NNNNNNTTN NTNTGCCCCG ATAACCTAG GNGACTTG AGATCCACCG	60
CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCgggntg CAGGACCCAA CGCTGCCCCG	120
GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT	180
GGTTTGCACA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA	240
T	241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCNCNC NNNNNTTTTN NGCAGCCCGT AATTACCCTC ACTNCCGGGA ACAAAGCTG	60
GGTACCGGGC CCCCCCTCGA GGTGACGGT ATCGATAAGC TTGATATCGA ATTCCTGCAG	120
TGTTTAAAAA ATAAAATAAA CTAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGTA	180
ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTTTACCC TAGTTACGGA AACACTAGAA	240
AGTCTTCACC CGGCCAAGAT AACACATCTT TAGTAAAAAT AGCAAGAAAT ATTTTATGGG	300
TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC	360
ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTTGGAGA CCAGNCTGGG	420
CAATGTGGNA AAACCTCATC TCCACTAAAA ATACAAAAAT TAGNCAGGCA TGGTGGTGCA	480
CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG	540
GGAGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT	600
TTCTTCCAAA AAAAAAAAAA AAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA	660

ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGNGTCA AGNGGGGCNG GCCACATGGG	720
GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGGG AGGACTNTAT CCNGTTCCGG	780
NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC	834

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 838 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTGGGCNCNC GCCCCTTAAN TTTTATNGN TTNCTANAAA AANANNNGGC NCNNTAAAT	60
ATATTTTTTN TTGTGACCCC TTTTAAAGG GACCCNCTAA AAAATTTTNT GGTTNNTTN	120
GATTTANGTG GGTGNTTTTN TTATATTTTT GNGAGNNTC TGTAGTCNTC NCCCTCAAAC	180
ANNTCNTACN ATNGGNANCG TGA CTCTGTC NTTNGTNANN NTCGNTNTCN NGTNATTENA	240
GGNNCCTCGC GCNNCNCGGG CNNNGTTTTT TTTNNCNNTT TTTAAGCCNA ANNCTCAGTA	300
NCNTCCAACG GNGCTNNGAC ANNGNNNCT NTCGNGGGTN CCCTCTNTNT NGNNCNNGGC	360
TNNNGNNNNC NGNCNGCNGN GCCNTGCGNN NNGNNNGNGG NNNGNTNCA TANGGATNGN	420
GNTGCTCNC NCNNGNGTNN TNAGTAGGNA NTTTTNTNNT ACTTGCCNNC NNNTNGCTGC	480
GAGNANAGCN ANNTNGNNGN AGNGNNGNTG CGCGGANNTT CCCCTGATNA NCTCGAGCNG	540
NTTACNGGNG CNNCCTNGAA NAAGNGNNGT ANNGTGCCGA GNCGCTANNC TGAGCCTGAG	600
TNTCGACNGG NATNGTGNT CNTACNGTTA NGGGNNGCNN GANCGGGNTG ANTCNCCGGN	660
NGANCNAGCG ACTGCCTNTC ANGCGAANC GTNCANGNN GTAGAGCANA GGGTNANNG	720
TCNNNNAAGC NTNNAGTGAN TGTCNTNACN NGTGANTTAC GGCNTAGNCT TGATNTNNAN	780
NCGAGGNNNN ATNNANNTT GGANANTTNN TNNNTCNCN TCGCGGNGNG NCNNGCCG	838

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 803 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTGCGCGGT AGCCCGATAA CTATAGGGCG ACNTGGAGNT CCACCGCGGT GGC GGCGCT	60
CTAGNAACTA GTGGATCCCC CGGGCTGCAG GAATTCACGG ACTAATCCTC TACAGATCTT	120
GCTGGAGTGG CCTTTCAGCC TTTTGTGACT GTTTGTAGTG AAATGTACAC ACAAGCCTAC	180

AAGGCAGCCC AGATGTACCA TAACTGTGGG AAAATTAAAA AAAAAAAAAAC ACAGAACCTC	240
TCTATGTTGC CCATGCTGGA CTCAACTCT TAGACAAGCA ATCCTCGTAC CTCAGCCTCC	300
TGAGTTCCTG AGTAGCTGGG ACTACAAGCA TGCACCACCA TGCCAGGCTA TGAGAAAGTT	360
CTTTTATTG ATCCAGACCT TATTGCCTGG TAACTTCCAC CACTGTTCTT AGCTCTGNTC	420
TCTGGTCCTA ACAGAGGAAA ATCTTGACCC CACACCTAGT GCAACTGGAT AGCTTATNGT	480
TGGGCTNGTG TTTCTCTAT TCTGGGTCCA CCCTAAAATC CNATAGATAC TCCAACGCT	540
CANAGNAAAC CAAGCTCTCT CTCTNNCTTN CTTTCTNNN CTCTATTNAT TNATGGGNNNA	600
TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAAATG GGGGAGGCAA	660
TCAATTTAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNNA	720
NGNNCNNCNC NNNCCNNTNN NNNGGTTTNN NNGNNNNGGG NNNCCNNNNN NANNNNNNTN	780
NNNCCNCCNA NNNTNCNNNN CCC	803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGGAACAAAA	60
GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA	120
ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAAGTT CTGTGTGCCA CACTGTTTTT	180
ATCTGTAAAA GGATAAAGGG AATATCATAA ATTAGNTTGT TAAGCCTTAG TTTAATAATG	240
TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTTCTTGT TTAGTGAATA ATCATTCTTA	300
TTATTTAATA GTATCTCTAC TAAATTTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC	360
GTGGTAATCA CTTCTGCTCA TATTTAACCT ATAAGCATAA TATAGTTTAT TTATATACCA	420
NTTATTTATT TTATTTTATT TGNNAGATG CAGCTTGTCT TTTNCAACCC AGGGNTGNGG	480
NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNC CAGGTNCAAG NGATTCTCCT	540
GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGGNTNT	600
NNGNTNGNNA GGNNNCACAN NNGNCAGGTN NNTCGNCTCC NNGCCANTNA CTNNNNCCAN	660
CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNNN NCNNNNNNNG GNGGANNCCN	720
NNTNGCNGNN ANNGNNANNN NNTNNNNNNN NNGGNCNNNG NNNNNNNNCC NNNNNNCCCC	780

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 803 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC	CNNNNNTTC	GNNCGTAACN	CGANTCACTA	TAGGGCGACT	TGGAGCTCCA	60
CCGCGGTGGC	GGCCGCTCTA	GAAGTAGTGG	ATCCCCCGGG	CTGCAGGAAT	TCGATATCAA	120
GCTTTNGTGT	GTAAAAAGTA	TTAGAATCTC	ATGTTTTTGA	ACAAGGTTGG	CAGTGGGTTG	180
GGAGGAGGGA	TTGGAGATTG	ATGCGATAGG	AATGTGAAGG	GATAGCTTGG	GGTGGATTTT	240
ATTTTTTAAT	TTTAATTTTT	ATTTNTTGTG	ATGGAGTCTT	GCTCTGTCTC	CCAGGCTGGA	300
GTGCAGTGGT	GTGATCTCAG	CTCACGGGTT	CAAGCGATTG	TCCTGCTGCA	GCCTCCCGAG	360
TAGCTGGGAT	TACAGGAGCG	CGCCACCACA	CCCGGNTAAT	TTNNTTGTAT	TTTTAGTAGA	420
GACGGGGTTT	CACCATGTTG	GTTAGGCTGG	TCTAGAACTC	CCAACCTCAT	GATCCGCCTG	480
CTTCGGCCTC	CCAAAGTGCC	GGAATTACAG	GCGTGAGCGA	CTGCACCCGG	CCGCTTGGGG	540
GTGGATTTTT	AAAGAAATTT	AGAAGAATGT	AACTTGGCCA	GATACCATGT	ACCCGTTAAT	600
TCATTTNCGG	TTTTTTGGAT	ACCCATTTTG	NNATTCTCCC	NCCACTGGAT	AAATAAGGGN	660
GGTTCATTNT	NGNTTAGTTT	GGGTNTTTTT	NAGTGTGGNT	TCTGCTTATN	ATTAGAATGG	720
NCTNCTTTNC	CAANCTGGAA	AGGGAGGAGT	TAAATCANT	ACCAGAANCA	GAAATTCTTT	780
TCANTTGTG	CNCNAGAAAT	GCC				803

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 819 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN	NNNNNAATTT	TNGCAGNCGC	GTAATTAACC	TCACTAAAGG	GAACAAAAGC	60
TGGGTACCGG	GGCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTCCCTCC	CCTTCCTCAG	120
CTCTGGCGAC	CCTGCGCTGT	GGTGGTTCTC	CAACCACACT	CATTCTCCTC	AGCTGGCTCC	180
TTGCTCTTCT	TCCACCCCCT	CGTTGGAAGT	GTTCTAAGT	GTTTGGCTTG	GCCTCCTCTT	240
CCCCTTCTT	AGNTTAGACT	TCTCCACTGC	TCCAACATCA	ACTGGAAATC	TATGGAATTG	300
ATTCTGTTT	TCAGCTCCAG	TCCTGTTTAC	AGGGCATTTT	CACCTGCTGG	CACTTCCAAA	360
GTGACACTTC	CAAACCACTT	CCTCGCCCTC	CTCTCTAAAC	CAGGTCTTTC	TTCCTAACTT	420



CCTTATTTCT GAGAATGTCT CTGNCATGTT CTAAACTGAA AACTCCTAGT CAACTNCACA	480
CTTTATTCCC TGGATCCTCA ATTGGGTTCC CATGTNCCGT TAGTGTTTCT TGGTAAGNCT	540
CTGCCANCAC CGNAGGATCG ACTCTAATCA CATCTCAACT GAATTATGGN AAAGTCAACT	600
CAATTCTCTC AACCATCCCA GGCTCCACTA TGGNTAATAT GCTAAGGAGA GCTGACCCAA	660
CGGGGAGAAG ATCTGNNGGG GAGGAGAGAA ACAAAGNTAA TGGAA TNATT CTCGAAAAGC	720
CCACAAGGNG AAGGATAACC CNCTTCCNCT CGAAAGAGGG GGGATCGCCA GATNTCGCGC	780
CCGGAAAGAA ACCGGGGNGA GGGGGTTACA NTGTAAGNC	819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG TACTGCTTGA GCAACTGGTG AAACTCCGCG CCTCACGCCC CGGGTGTGTC	60
CTTGTCAGG GCGACGAGC ATTCTGGGCG AAGTCCGCAC GCCTCTTGTT CGAGGCGGAA	120
GACGGGGTCT GATGCTTTCT CCTTGGTCGG GACTGTCTCG AGGCATGCAT GTCCAGTGAC	180
TCTTGTGTTT GCTGCTGCTT CCCTCTCAGA TTCTTCTCAC CGTTGTGGTC AGCTCTGCTT	240
TAGGCATATT AATCCATAGT GGAGGCTGGG ATGGGTGAGA GAATTGAGGT GACTTTTCCA	300
TAATTCAGGT GAGATGTGAT TAGAGTTCGA TCTGCGGTGG TGGCAGAGGC TTACAAGAAA	360
CACTAACGGG ACATGGGAAC CAATTGAGGA TCAGGGAATA AAGTGTGAAG TTGACTAGGA	420
GGTTTTTCAGT TTAGAACATG GCAGAGACAT TCTCAGAAAT AAGGAAGTTA GGAAGAAAGA	480
CTGGTTTAGA GAGGAGGGCG ANGAAGTGGT TTGGGAAGTG TCACTTTGGG AAGTGCCAGC	540
AGGTGAAAAT GCCTGTGACA GGATGGAGCT GAAAACAGGA TCAATTCCAT AGATTCCAGT	600
TGATGTNGGA GCAGGGGAGA AGTCTTAGCT AAGGAAGGGG AAGAGGAGGC CAAGGNAACA	660
CTTAGGACAA TTGNAACGAN GGGGGGGGAG AAGAGNAAGG GCCACTTAGG GGAATAATNT	720
GGTGGGGGAC CCCCAAGNNA GGGCGCANNN TTAGGAGGGG GGGANNTCAN AGGAAAGTGG	780
AAGNTTGGGT TTANCT	796

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTCGTCGTA NCCCGATNAC TATAGGGCGA CTTGGAGCTC CACCGCGGTG GCGGNCGCGG	60
GCAGGGNCCG GNCCTTTGTG GCCGCCCCGG CCGCGAAGCC GGTGTCCTAA AAGATGAGGG	120
GCGGGGCGCG GNCGGTTGGG GCTGGGGAAC CCCGTGTGGG AAACCAGGAG GGGCGGCCCCG	180
TTTCTCGGGC TTCGGGCGCG GCCGGGTGGA GAGAGATTCC GGGGAGCCTT GTCCCGAAA	240
TGCTGTTTGC TCGAAGACGT CTCAGGGCGC AGGTGCCTTG GGCCGGGATT AGTAGCCGTC	300
TGAACTGGAG TGGAGTAGGA GAAAGAGGAA GCGTCTTGGG CTGGGTCTGC TTGAGCAACT	360
GGTGAAACTC CGCGCCTCAC GCCCCGGGTG TGTCTTGTG CAGGGGCGAC GAGCATTCTG	420
GGCGAAGTCC GCACGCCTCT TGTTCGAGGC GGAAGACGGG GTCTTGATGC TTTCTCCTTG	480
GGTCGGGGAC TGTCTCGAGG CATGCATGTC CAGTGA CTCT TGTGTTTGGT GNTGCTTCCC	540
TCTCAGATCT TCTCACCGNG GTGGGCAACT CTGTTTAGGC ATATTATCCA TAGNGGAGGC	600
TGGATGGTTG AAANAATTGA GGTNATTTTC CATAATCAAG TGAAATTTGA TAGAGTCCGN	660
CTTTNGGGGT GNAAGGGTTA AAAAAAATA ACGGAAATGG AACAATGAGG TCAAGGATTA	720
GTTGAGTTGN TAGNGGTTCA ATTAGANATG AAGGNATCTA AAATAGGAGT AGAGAANNNG	780
TTNAAAGAGG GAAAATTTTG CC	802

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC GCGTAATTAA CCTCACTAAA GGAACAAAA GCTGGGTACC GGGCCCCCCC	60
TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCT GCAGCCCGGG GGATCCGCCC	120
CGCGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC CGCCCGGGN CTCACATTTT	180
ATTTCTATTG GCTAGCGCTG CTCTAAATCT TCTGTTCCCT CTGCTACACC AGGCCTAACA	240
CTCAAAATCC CTGCCAACCT TTTCTTCCT GAAGCTTCCC TCCCCTTCCT CAGCTCTGGC	300
GACCCTGCGC TGTGGTGGTT CTCCAACCAC ACTCATTCTC CTCAGCTGGC TCCTTGCTCT	360
TCTTCCACCC CCTCGNTGGA AGTGTTCTTA AGTGTTCGGC TTGGCCTCCT CTTCCCCCTT	420
CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCCTG	480
TTTCAGCTCC AGTCCTGTTC ACAGGGGATT TTCANCTGGT GGCATTTCCA AAGTGAAATT	540
CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC	600
TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTTATCCC	660

TGATCCCAAA TGGTCCCATT CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTCGGANTT TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG CTAAGAGGGT NCC	720 780 793
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(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 440 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCTTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG	60
AGAGTGTTAC AGTCTAATTC TATATCACAT GTAACCTTTA TTTGGATATA TCAGTAATAG	120
TGCTTTTTCN TTTTTTTTTT TTNTTTTTTT TNNTTTTNGG GGANAGAGTC TCGCTCTGTC	180
GCCAGGTTGG AGTGCAATGG TCGGATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTCA	240
AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGGACTA CAGGGGTGCG CCACCACGCC	300
TGGGATAATT TTGGGNTTTT TAGTAGAGAT GCGGTTTCAC CANCTTGGNG CAGGCTGGTC	360
TTGGAACTCC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG	420
GGGTGAGCCA CTGTTCTTGG	440

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC	60
TCTTAATGTC AAAACTTTGA TTACACAGTC CCTTTAAGGC AGTTCTGTTT TAACCCCAGG	120
TGGGTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT	180
TCTCTACCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAACTGTA AGCTCTGCCC	240
TGAGATATTC TTA CTCAATT TAATTGTGTA GTTTTTAAAA TTCCCCAGGA AATTCTGGTA	300
TTTCTGTTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT	360
GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT	420
GAGAGTTTGG GTGGNGGTTT NGNATTTAAT GAC	453

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 369 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AAACCTCAATC ACAAGTCTGG	60
GTTTTTAACA TAGTAACTG AATATTTCCC TTGGGGGGTT AAATTTTAGA ACAGACGTNC	120
ATNCAATCTG GAAGAAGAGC TATGAAAAA ACCTAGCTTG GGTNGGTTTC ATAGGGTNCA	180
TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA	240
GTAAACTAC TTGGAAAAA NTTAAAAGAT ACAGAAATTT CTATCTTAAA TGATGTGTGG	300
GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCCAGAGG TGAAGAGNAT NCTCTATGCT	360
GTGNGGGGGG	369

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 516 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG CTTACGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCCG CACAGCATAG AGAAGCCCC GCACAGCATA	120
GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTTAATTTY TTTTMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC	420
CCCCCAGGGA AATATTCAGT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTTGCC	480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC	516

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA GGTGCTATAA GGTGAGCATG AGACACAGAT CTTTGCTTTC CACCCTGTTC	60
TTCTTATGGT TGGGTATTCT TGTCACAGTA ACTTAACTGA TCTAGGAAAG AAAAAATGTT	120
T	121

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAC	18
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(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T	21
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(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT	19
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(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G 21

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC 19

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC 19

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2791 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCAAT GACAGAGTTA CCTGCACCGT TGTCCTACTT CCAGAATGCA CAGATGTCTG	300

AGGACAACCA	CCTGAGCAAT	ACTGTACGTA	GCCAGAATGA	CAATAGAGAA	CGGCAGGAGC	360
ACAACGACAG	ACGGAGCCTT	GGCCACCCTG	AGCCATTATC	TAATGGACGA	CCCCAGGGTA	420
ACTCCCGGCA	GGTGGTGGAG	CAAGATGAGG	AAGAAGATGA	GGAGCTGACA	TTGAAATATG	480
GCGCCAAGCA	TGTGATCATG	CTCTTTGTCC	CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	540
CTACCATTAA	GTCAGTCAGC	TTTTATACCC	GGAAGGATGG	GCAGCTAATC	TATACCCCAT	600
TCACAGAAGA	TACCGAGACT	GTGGGCCAGA	GAGCCCTGCA	CTCAATTCTG	AATGCTGCCA	660
TCATGATCAG	TGTCATTGTT	GTCATGACTA	TCCTCCTGGT	GGTTCTGTAT	AAATACAGGT	720
GCTATAAGGT	CATCCATGCC	TGGCTTATTA	TATCATCTCT	ATTGTTGCTG	TTCTTTTTTT	780
CATTCATTTA	CTTGGGGGAA	GTGTTTAAAA	CCTATAACGT	TGCTGTGGAC	TACATTACTG	840
TTGCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	TTCCATTAC	TGGAAAGGTC	900
CACTTCGACT	CCAGCAGGCA	TATCTCATT	TGATTAGTGC	CCTCATGGCC	CTGGTGTTTA	960
TCAAGTACCT	CCCTGAATGG	ACTGCGTGGC	TCATCTTGGC	TGTGATTTC	GTATATGATT	1020
TAGTGGCTGT	TTTGTGTCCG	AAAGGTCCAC	TTCGTATGCT	GGTTGAAACA	GCTCAGGAGA	1080
GAAATGAAAC	GCTTTTTCCA	GCTCTCATTT	ACTCCTCAAC	AATGGTGTGG	TTGGTGAATA	1140
TGGCAGAAGG	AGACCCGGAA	GCTCAAAGGA	GAGTATCCAA	AAATTCCAAG	TATAATGCAG	1200
AAAGCACAGA	AAGGGAGTCA	CAAGACACTG	TTGCAGAGAA	TGATGATGGC	GGGTTCAGTG	1260
AGGAATGGGA	AGCCCAGAGG	GACAGTCATC	TAGGGCCTCA	TCGCTCTACA	CCTGAGTCAC	1320
GAGCTGCTGT	CCAGGAACTT	TCCAGCAGTA	TCCTCGCTGG	TGAAGACCCA	GAGGAAAGGG	1380
GAGTAAAACT	TGGATTGGGA	GATTTCATTT	TCTACAGTGT	TCTGGTTGGT	AAAGCCTCAG	1440
CAACAGCCAG	TGGAGACTGG	AACACAACCA	TAGCCTGTTT	CGTAGCCATA	TTAATTGGTT	1500
TGTGCCTTAC	ATTATTACTC	CTTGCCATTT	TCAAGAAAGC	ATTGCCAGCT	CTTCCAATCT	1560
CCATCACCTT	TGGGCTTGTT	TTCTACTTTG	CCACAGATTA	TCTTGACAG	CCTTTTATGG	1620
ACCAATTAGC	ATTCCATCAA	TTTTATATCT	AGCATATTTG	CGGTTAGAAT	CCCATGGATG	1680
TTTCTTCTTT	GACTATAACC	AAATCTGGGG	AGGACAAAGG	TGATTTTCCT	GTGTCCACAT	1740
CTAACAAAGT	CAAGATTCCC	GGCTGGACTT	TTGCAGCTTC	CTTCCAAGTC	TTCTTGACCA	1800
CCTTGCACTA	TTGGACTTTG	GAAGGAGGTG	CCTATAGAAA	ACGATTTTGA	ACATACTTCA	1860
TCGCAGTGGA	CTGTGTCCCT	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920
GATATGATAG	GCCCGGAAGT	TGCTGTGCCC	CATCAGCAGC	TTGACGCGTG	GTCACAGGAC	1980
GATTTCA <del>G</del> TG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040
TTTAAACCAA	ACGGAACTCT	TCATCTTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100
GTATTAACTG	AATTCTGAAC	TTTTCAGGAG	GTA <del>C</del> TGTGAG	GAAGAGCAGG	CACCAGCAGC	2160
AGAATGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220

CTCATCCTTT TTAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA	2280
TTGCCTTTGG CAATTCCTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT	2340
TCTTCCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTTA ACCTCAGGTT	2400
CCAAATTCAG TAAATTTTGG AAACAGTACA GCTATTTCTC ATCAATTCTC TATCATGTTG	2460
AAGTCAAATT TGGATTTTCC ACCAAATTCT GAATTTGTAG ACATACTTGT ACGCTCACTT	2520
GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCCAC ACAAGCAGTC TTTTCTACA	2580
GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	1	5	10	15
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	20	25	30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	35	40	45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	50	55	60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	65	70	75	80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	85	90	95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	100	105	110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	115	120	125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	130	135	140	
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	145	150	155	160
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe	165	170	175	



Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	
			180					185					190			
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val	
		195					200					205				
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	
	210					215					220					
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	
225					230					235					240	
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr	
				245					250					255		
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	
			260					265					270			
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr	
		275					280					285				
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu	
	290					295					300					
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	Tyr	Asn	Ala	Glu	Ser	Thr	
305					310					315					320	
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe	
				325					330					335		
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg	
			340					345					350			
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile	
		355					360					365				
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	
	370					375					380					
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala	
385					390					395					400	
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	
				405					410					415		
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu	
			420					425					430			
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala	
		435					440					445				
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln	
	450					455					460					
Phe	Tyr	Ile														
465																

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1964 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC	GGCAGCTGAG	GCGGAAACCT	AGGCTGCGAG	CCGGCCGCCC	GGGCGCGGAG	60
AGAGAAGGAA	CCAACACAAG	ACAGCAGCCC	TTCGAGGTCT	TTAGGCAGCT	TGGAGGAGAA	120
CACATGAGAG	AAAGAATCCC	AAGAGGTTTT	GTTTTCTTTG	AGAAGGTATT	TCTGTCCAGC	180
TGCTCCAATG	ACAGAGATAC	CTGCACCTTT	GTCCTACTTC	CAGAATGCCC	AGATGTCTGA	240
GGACAGCCAC	TCCAGCAGCG	CCATCCGGAG	CCAGAATGAC	AGCCAAGAAC	GGCAGCAGCA	300
GCATGACAGG	CAGAGACTTG	ACAACCCTGA	GCCAATATCT	AATGGGCGGC	CCCAGAGTAA	360
CTCAAGACAG	GTGGTGAAC	AAGATGAGGA	GGAAGACGAA	GAGCTGACAT	TGAAATATGG	420
AGCCAAGCAT	GTCATCATGC	TCTTTGTCCC	CGTGACCCTC	TGCATGGTCG	TCGTCGTGGC	480
CACCATCAAA	TCAGTCAGCT	TCTATACCCG	GAAGGACGGT	CAGCTAATCT	ACACCCCATT	540
CACAGAAGAC	ACTGAGACTG	TAGGCCAAAG	AGCCCTGCAC	TCGATCCTGA	ATGCGGCCAT	600
CATGATCAGT	GTCATTGTCA	TTATGACCAT	CCTCCTGGTG	GTCCTGTATA	AATACAGGTG	660
CTACAAGGTC	ATCCACGCCT	GGCTTATTAT	TTCATCTCTG	TTGTTGCTGT	TCTTTTTTTC	720
GTTTATTTAC	TTAGGGGAAG	TATTTAAGAC	CTACAATGTC	GCCGTGGACT	ACGTTACAGT	780
AGCACTCCTA	ATCTGGAATT	TTGGTGTGGT	CGGGATGATT	GCCATCCACT	GGAAAGGCCC	840
CCTTCGACTG	CAGCAGGCGT	ATCTCATTAT	GATCAGTGCC	CTCATGGCCC	TGGTATTTAT	900
CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTTGGCT	GTGATTTTCA	TATATGATTT	960
GGTGGCTGTT	TTATGTCCCA	AAGGCCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTTCCAG	CTCTTATCTA	TTCCTCAACA	ATGGTGTGGT	TGGTGAATAT	1080
GGCTGAAGGA	GACCCAGAAG	CCCAAAGGAG	GGTACCCAAG	AACCCCAAGT	ATAACACACA	1140
AAGAGCGGAG	AGAGAGACAC	AGGACAGTGG	TTCTGGGAAC	GATGATGGTG	GCTTCAGTGA	1200
GGAGTGGGAG	GCCCAAAGAG	ACAGTCACCT	GGGGCCTCAT	CGCTCCACTC	CCGAGTCAAG	1260
AGCTGCTGTC	CAGGAACTTT	CTGGGAGCAT	TCTAACGAGT	GAAGACCCGG	AGGAAAGAGG	1320
AGTAAAACTT	GGACTGGGAG	ATTTTATTTT	CTACAGTGTT	CTGGTTGGTA	AGGCCTCAGC	1380
AACCGCCAGT	GGAGACTGGA	ACACAACCAT	AGCCTGCTTT	GTAGCCATAC	TGATCGGCCT	1440
GTGCCTTACA	TTACTCTGTC	TCGCCATTTT	CAAGAAAGCG	TTGCCAGCCC	TCCCCATCTC	1500
CATCACCTTC	GGGCTCGTGT	TCTACTTCGC	CACGGATTAC	CTTGTGCAGC	CCTTCATGGA	1560
CCAACCTGCA	TTCCATCAGT	TTTATATCTA	GCCTTTCTGC	AGTTAGAACA	TGGATGTTTC	1620
TTCTTTGATT	ATCAAAAACA	CAAAAACAGA	GAGCAAGCCC	GAGGAGGAGA	CTGGTGACTT	1680
TCCTGTGTCC	TCAGCTAACA	AAGGCAGGAC	TCCAGCTGGA	CTTCTGCAGC	TTCTTCCGA	1740
GTCTCCCTAG	CCACCCGCAC	TACTGGACTG	TGGAAGGAAG	CGTCTACAGA	GGAACGGTTT	1800

CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA 1860  
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GACCGTGGGC ATGGAGATTT 1920  
ACCCGCACTG TGAACCTCTCT AAGGTAAACA AAGTGAGGTG AACC 1964

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 467 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Thr	Glu	Ile	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Ser	His	Ser	Ser	Ser	Ala	Ile	Arg	Ser	Gln	Asn	Asp	Ser	20	25	30	
Gln	Glu	Arg	Gln	Gln	Gln	His	Asp	Arg	Gln	Arg	Leu	Asp	Asn	Pro	Glu	35	40	45	
Pro	Ile	Ser	Asn	Gly	Arg	Pro	Gln	Ser	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Ile	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	180	185	190	
Val	Asp	Tyr	Val	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val	195	200	205	
Gly	Met	Ile	Ala	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	210	215	220	

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 225 230 235 240  
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 245 250 255  
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 260 265 270  
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 275 280 285  
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 290 295 300  
 Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala  
 305 310 315 320  
 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe  
 325 330 335  
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 340 345 350  
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile  
 355 360 365  
 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 370 375 380  
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 385 390 395 400  
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
 405 410 415  
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
 420 425 430  
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
 435 440 445  
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln  
 450 455 460  
 Phe Tyr Ile  
 465

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCA CGAGGGCATT TCCAGCAGTG AGGAGACAGC CAGAAGCAAG CTTTGGAGC

TGAAGGAACC	TGAGACAGAA	GCTAGTCCCC	CCTCTGAATT	TTACTGATGA	AGAAACTGAG	120
GCCACAGAGC	TAAAGTGA	TTTCCCAAGG	TCGCCCAGCG	AGGACGTGGG	ACTTCTCAGA	180
CGTCAGGAGA	GTGATGTGAG	GGAGCTGTGT	GACCATAGAA	AGTGACGTGT	TAAAAACCAG	240
CGCTGCCCTC	TTTGAAAGCC	AGGGAGCATC	ATTCATTTAG	CCTGCTGAGA	AGAAGAAACC	300
AAGTGTCGGG	GATTCAAGAC	CTCTCTGCGG	CCCCAAGTGT	TCGTGGTGCT	TCCAGAGGCA	360
GGGCTATGCT	CACATTCATG	GCCTCTGACA	GCGAGGAAGA	AGTGTGTGAT	GAGCGGACGT	420
CCCTAATGTC	GGCCGAGAGC	CCCACGCCGC	GCTCCTGCCA	GGAGGGCAGG	CAGGGCCCAG	480
AGGATGGAGA	GAATACTGCC	CAGTGGAGAA	GCCAGGAGAA	CGAGGAGGAC	GGTGAGGAGG	540
ACCCTGACCG	CTATGTCTGT	AGTGGGGTTC	CCGGGCGGCC	GCCAGGCCCTG	GAGGAAGAGC	600
TGACCCTCAA	ATACGGAGCG	AAGCATGTGA	TCATGCTGTT	TGTGCCCTGTC	ACTCTGTGCA	660
TGATCGTGGT	GGTAGCCACC	ATCAAGTCTG	TGCGCTTCTA	CACAGAGAAG	AATGGACAGC	720
TCATCTACAC	GCCATTCACT	GAGGACACAC	CCTCGGTGGG	CCAGCGCCTC	CTCAACTCCG	780
TGCTGAACAC	CCTCATCATG	ATCAGCGTCA	TCGTGGTTAT	GACCATCTTC	TTGGTGGTGC	840
TCTACAAGTA	CCGCTGCTAC	AAGTTCATCC	ATGGCTGGTT	GATCATGTCT	TCACTGATGC	900
TGCTGTTTCT	CTTCACCTAT	ATCTACCTTG	GGGAAGTGCT	CAAGACCTAC	AATGTGGCCA	960
TGGACTACCC	CACCCTCTTG	CTGACTGTCT	GGAACCTCGG	GGCAGTGGGC	ATGGTGTGCA	1020
TCCACTGGAA	GGGCCCTCTG	GTGCTGCAGC	AGGCCACCT	CATCATGATC	AGTGCGCTCA	1080
TGGCCCTAGT	GTTCATCAAG	TACCTCCCAG	AGTGGTCCGC	GTGGGTCATC	CTGGGCGCCA	1140
TCTCTGTGTA	TGATCTCGTG	GCTGTGCTGT	GTCCCAAAGG	GCCTCTGAGA	ATGCTGGTAG	1200
AAACTGCCCA	GGAGAGAAAT	GAGCCCATAT	TCCCTGCCCT	GATATACTCA	TCTGCCATGG	1260
TGTGGACGGT	TGGCATGGCG	AAGCTGGACC	CCTCCTCTCA	GGGTGCCCTC	CAGCTCCCCT	1320
ACGACCCGGA	GATGGAAGAA	GACTCCTATG	ACAGTTTTGG	GGAGCCTTCA	TACCCCGAAG	1380
TCTTTGAGCC	TCCCTTGA	GGCTACCCAG	GGGAGGAGCT	GGAGGAAGAG	GAGGAAAGGG	1440
GCGTGAAGCT	TGGCCTCGGG	GACTTCATCT	TCTACAGTGT	GCTGGTGGGC	AAGGCGGCTG	1500
CCACGGGCAG	CGGGGACTGG	AATACCACGC	TGGCCTGCTT	CGTGGCCATC	CTCATTGGCT	1560
TGTGTCTGAC	CCTCCTGCTG	CTTGCTGTGT	TCAAGAAGGC	GCTGCCC GCC	CTCCCCATCT	1620
CCATCACGTT	CGGGCTCATC	TTTTACTTCT	CCACGGACAA	CCTGGTGCGG	CCGTTCATGG	1680
ACACCCTGGC	CTCCCATCAG	CTCTACATCT	GAGGGACATG	GTGTGCCACA	GGCTGCAAGC	1740
TGCAGGGAAT	TTTCATTGGA	TGCAGTTGTA	TAGTTTTACA	CTCTAGTGCC	ATATATTTTT	1800
AAGACTTTTT	TTTCCTTAAA	AAATAAAGTA	CGTGTTTACT	TGGTGAGGAG	GAGGCAGAAC	1860
CAGCTCTTTG	GTGCCAGCTG	TTTCATCACC	AGACTTTGGC	TCCCGCTTTG	GGGAGCGCCT	1920
CGCTTCACGG	ACAGGAAGCA	CAGCAGGTTT	ATCCAGATGA	ACTGAGAAGG	TCAGATTAGG	1980

GTGGGGAGAA GAGCATCCGG CATGAGGGCT GAGATGCCCA AAGAGTGTGC TCGGGAGTGG	2040
CCCCTGGCAC CTGGGTGCTC TGGCTGGAGA GGAAAAGCCA GTTCCCTACG AGGAGTGTTT	2100
CCAATGCTTT GTCCATGATG TCCTTGTTAT TTTATTNCCY TTANAAACTG ANTCCTNTTN	2160
TTNTTDCGGC AGTCACMCTN CTGGGRAGTG GCTTAATAGT AANATCAATA AANAGNTGAG	2220
TCCTNTTAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
AAAAA	2285

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Leu	Thr	Phe	Met	Ala	Ser	Asp	Ser	Glu	Glu	Glu	Val	Cys	Asp	Glu	1	5	10	15
Arg	Thr	Ser	Leu	Met	Ser	Ala	Glu	Ser	Pro	Thr	Pro	Arg	Ser	Cys	Gln	20	25	30	
Glu	Gly	Arg	Gln	Gly	Pro	Glu	Asp	Gly	Glu	Asn	Thr	Ala	Gln	Trp	Arg	35	40	45	
Ser	Gln	Glu	Asn	Glu	Glu	Asp	Gly	Glu	Glu	Asp	Pro	Asp	Arg	Tyr	Val	50	55	60	
Cys	Ser	Gly	Val	Pro	Gly	Arg	Pro	Pro	Gly	Leu	Glu	Glu	Glu	Leu	Thr	65	70	75	80
Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	85	90	95	
Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	Val	Arg	Phe	Tyr	100	105	110	
Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	115	120	125	
Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	Asn	Thr	Leu	Ile	130	135	140	
Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	Val	Val	Leu	Tyr	145	150	155	160
Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	Ile	Met	Ser	Ser	165	170	175	
Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	Gly	Glu	Val	Leu	180	185	190	

Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	Leu	Leu	Thr	Val
		195					200					205			
Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	Trp	Lys	Gly	Pro
		210				215					220				
Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala
225					230					235					240
Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	Trp	Val	Ile	Leu
				245					250					255	
Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly
			260					265					270		
Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Pro	Ile
		275					280					285			
Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp	Thr	Val	Gly	Met
	290					295					300				
Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	Leu	Pro	Tyr	Asp
305					310					315					320
Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	Glu	Pro	Ser	Tyr
				325					330					335	
Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro	Gly	Glu	Glu	Leu
			340					345					350		
Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	Asp	Phe	Ile
		355					360					365			
Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Asp
	370					375					380				
Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	Gly	Leu	Cys
385					390					395					400
Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala	Leu	Pro	Ala	Leu
				405					410					415	
Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe	Ser	Thr	Asp	Asn
			420					425					430		
Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His	Gln	Leu	Tyr	Ile
		435					440					445			

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C

31

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC

25

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG

24

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTTGAAT TCTTAGGCTA TGGTTGTGTT CCA

33

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTTCC TTTAGTCTCT	60
CTTAAAGAGT GAGAAAAATT TTCCAGGAA TCCCGGTGGA CTTTGCTTCA CCACTCATAG	120
GTTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTTG TTAGGAAGAG GCTTGGTGGG	180
ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCACCA GAGTCATGTG GGAGGGGGTG	240
GGAACCCAAA CAATTCAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATA GCTGTTGGAT	300

AAACTACCAG CAGGCACTGC TACAGCCCAT GCTTTGTGGT TTAAGGGCCA GCTAGTTACA	360
ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT	420
TAGAGCTGTA ACTTCCACTT TCTCTTGAAG GCACAGWAAG GGAGTCACAA GACACTGTTG	480
CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCATCTAG	540
GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRAC TTTC ANCAGTATCC	600
TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATNTTTCAAA GTCATGGATT	660
CCTTTAGGTA GCTACATTAT CAACCTTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT	720
CTAATTCTAT ATCACATGTA ACTTTTATTT GGATATATCA GTAATAGTGC TTTTTYNTTT	780
TTTTTTTTTT TTTTTTTTTT TTTTNGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT	840
GCAATGGTGC GATCTTGGCT CACTGAAAGC TCCACCNCCC GGGTTCAAGT GATTCTCCTG	900
CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTTG	960
GGNTTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA	1020
NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG	1080
TTCTGGGCC TC	1092

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT	60
CTCCCAAAAA AAAAAATAT TAATTAATAT GATNAAATGA TGCCTATCTC AGAATTCTTG	120
TAAGGATTTT TTAGKACAAG TGCTGGGTAT AAATATANA TTCRATAGAT GNCGATTATT	180
ACTTAYTATT GTTATTGATA AATAACAGCA GCATCTACAG TTAAGACTCC AGAGTCAGTC	240
ACATAGAATC TGGNACTCCT ATTGTAGNAA ACCCNMMAG AAAGAAAACA CAGCTGAAGC	300
CTAATTTTGT ATATCATTTA CTGACTTCTC TCATTCATTG TGGGGTTGAG TAGGGCAGTG	360
ATATTTTGA ATTGTGAAAT CATANCAAAG AGTGACCAAC TTTTAAATAT TTGTAACCTT	420
TCCTTTTLAG GGGGAGTAAA ACTTGGATTG GGAGATTTCA TTTTCTACAG TGTTCTGGTT	480
GGTAAAGCCT CAGCAACAGC CAGTGGAGAC TGGAACACAA CCATAGCCTG TTTCGTAGCC	540
ATATTAATTG TMMSTATACA CTAATAAGAA TGTGTCAGAG CTCTTAATGT CMAAACTTTG	600
ATTACACAGT CCCTTTAAGG CAGTTCTGTT TTAACCCAG GTGGGTAAA TATTCCAGCT	660
ATCTGAGGAG CTTTTNGATA ATTGGACCTC ACCTTAGTAG TTCTCTACCC TGGCCACACA	720

TTAGAATCAC TTGGGAGCTT TTAAAACTGT AAGCTCTGCC CTGAGATATT CTTACTCAAT	780
TTAATTGTGT AGTTTTTAAA ATTCCCCAGG AAATTCCTGGT ATTTCTGTTT AGGAACCGCT	840
GCCTCAAGCC TAGCAGCACA GATATGTAGG AAATTAGCTC TGTAAGGTTG GTCTTACAGG	900
GATAACAGA TCCTTCCTTA GTCCCTGGAC TTAATCACTG AGAGTTTGGG TGGTGGTTTT	960
GGATTTAATG ACACAACCTG TAGCATGCAG TGTTACTTAA GAC	1003

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC CCTTTTGTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGTTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGCAA TTMAGNCCA	300
GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA	360
CGCCYCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA	480
ACAAGTTTTT ATGCAGGTGT CAGTATTTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTTA AACTGCATAC TTCCTGTACA	660
TTGTTTTTTC TTGCTTCAGG TTTTGTAGA TCATAGTGAC GGGTCTGTTG TTAATCCCAG	720
GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT	840
GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260

ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCTTNC TNACTTKGN GGATTAAATT	1380
CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTTCC TTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTG GGACAAGGGA GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1883 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTCNCCAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCCTGG AGACCATATG ACCCATAGAG CTAAATATAT TCAGTCTGGC TTTTACAGA	240
GATGTTTCTG ACTTTGTAA TAGAAAATCA ACCCAACTGG TTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTACGTTT	360
ATCCAAGGAC TCAATCTCCT TCTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480
ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600
CTKKNTGGCT GGGAATATTG GCACCTGGAA TAAAATGTT TTTCTGTGAA TGAGAAACAA	660
GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACTCCA GTTGCAATTA CTCTGCAGAT	720
GAGAGGCACT AATTATAAGC CATATTACCT TTCTTCTGAC AACCCTTGT CAGCCNCGT	780
GGTTTCTGTG GCAGAATCTG GTTCYATAMC AAGTTCCTAA TAANCTGTAS CCNAAAAAAT	840
TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC	900
TTACATGTT AAGTCCTTCT TTCCATATGT TAGACATTTT CTTTGAAGCA ATTTTAGAGT	960
GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA	1020
CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTGAGGT GGTAAATGTGG	1080

KTGGTGATCT YCATTAAACAC TGANCTAGGG CTTTKGKGTT TGKTTTATTG TAGAATCTAT	1140
ACCCCATTC A NAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT	1200
GCTGCCATCA TGATCAGNGT CATTGTWGTG ATGACTANNC TCCTGGTGGT TCWGTATAAA	1260
TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTTGN TTTCCACCCT GTTCTTCTTA	1320
TGGTTGGGTA TTCTTGTCAC AGTAACTTAA CTGATCTAGG AAAGAAAAAA TGTTTTGTCT	1380
TCTAGAGATA AGTTAATTTT TAGTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCCAGG AGTTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA	1560
AAACAAAAAA CAAATATTGG AAGTATTTTA TATGCATGGA ATCTATATGT CATGAAAAAA	1620
TTAGTGTAAT ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTTT AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA	1740
AGTTGTAAC T GAAAAATAAA CATTTCATA TAATAGCACA ATCTAAGTGG GTTTTTGN TT	1800
GTTTGTTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA ATTTCTCCGT TCCACCCTTG ATTAAATAAG GTAGTATTCA TTTTTTAAGT	60
TTTAGCTTTT GGATATATGT GTAAGTGTGG TATGCTGTCT AATGAATTAA GACAATTGGT	120
NCTKTCTTTA CCCMACANCT GGACMAAGAG CAGGCAAGAT NCAANAATCA AGTGACCCAG	180
NCAAACCAGA CACATTTTCT GCTCTCAGCT AGCTTGCCAC CTAGAAAGAC TGGTTGTCNA	240
AGTTGGAGTC CAAGAATCGC GGAGGATGTT TAAAATGCAG TTTCTCAGGT TCTCNCCACC	300
CACCAGAAGT TTTGATTCAT TGAGTGGTGG GAGAGGGCAG AGATATTTGC GATTTTAACA	360
GCATTCTCTT GATTGTGATG CAGCTGGTTC SCAAATAGGT ACCCTAAAGA AATGACAGGT	420
GTAAATTTA GGATGGCCAT CGCTTGATG CCGGGAGAAG CACACGCTGG GCCCAATTTA	480
TATAGGGGCT TTCGTCCTCA GCTCGAGCAR CCTCAGAACC CCGACAACCY ACGCCAGCKC	540
TCTGGGCGGA TTCCRTCAGK TGGGGAAGSC CAGGTGGAGC TCTGGKTTCT CCCC GCAATC	600
GTTTCTCCAG GCCGGAGGCC CCGCCCCCTT CCTCCTGGCT CCTCCCCTCC TCCGTGGGCC	660

GNCCGCCAAC GACGCCAGAG CCGGAAATGA CGACAACGGT GAGGGTTCTC GGGCGGGGCC	720
TGGGACAGGC AGCTCCGGGG TCCNCGNNWT NACATCGGAA ACAAACAGC GGCTGGTCTG	780
GAAGGAACCT GAKCTACGAC CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATGTGCGTG	840
ATGGGGAGTC CGGGCAAGCC AGGAAGGCAC CGCGGACATG GGCGGCCGCG GGCAGGGNCC	900
GGNCCTTTGT GGCCGCCCCG GCCGCGAAGC CGGTGTCCTA AAAGATGAGG GGCGGGGCGC	960
GGCCGGTTGG GGCTGGGGAA CCCC GTGTGG GAAACCAGGA GGGGCGGCC GTTTCTCGGG	1020
CTTCGGGCGC GGCCGGGTGG AGAGAGATTC CGGGGAGCCT TGGTCCGGAA ATGCTGTTTG	1080
CTCGAAGACG TCTCAGGGCG CAGGTGCCTT GGGCCGGGAT TAGTAGCCGT CTGAACTGGA	1140
GTGGAGTAGG AGAAAGAGGA AGCGTCTTGG GCTGGGTCTG CTTGAGCAAC TGGTGAAACT	1200
CCGCGCCTCA CGCCCCGGGT GTGTCCTTGT CCAGGGGCGA CGAGCATTCT GGGCGAAGTC	1260
CGCACGCCTC TTGTTGAGG CGGAAGACGG GGTCTTGATG CTTTCTCCTT GGTGCGGACT	1320
GTCTCGAGGC ATGCATGTCC AGTGACTCTT GTGTTTGCTG CTGCTCCCT CTCAGATTCT	1380
TCTCACCGTT GTGGTCAGCT CTGCTTTAGG CATATTAATC CATAGTGGAG GCTGGGATGG	1440
GTGAGAGAAT TGAGGTGACT TTTCCATAAT TCAGGTGAGA TGTGATTAGA GTYCGGATCC	1500
TNCGGTGGTG GCAGAGGCTT ACCAAGAAAC ACTAACGGGA CATGGGAACC AATTGAGGAT	1560
CCAGGGAATA AAGTGTGAAG TTGACTAGGA GGTTTTCAGT TTAAGAACAT GGCAGAGACA	1620
TTCTCAGAAA TAAGGAAGTT AGGAAGAAAG ACCTGGTTTA GAGAGGAGGG CGAGGAAGTG	1680
GTTTGGAAGT GTCACTTTGG AAGTGCCAGC AGGTGAAAT GCCCTGTGAA CAGGACTGGA	1740
GCTGAAAACA GGAATCAATT CCATAGATTT CCAGTTGATG TTGGAGCAGT GGAGAAGTCT	1800
AANCTAAGGA AGGGGAAGAG GAGGCCAAGC CAAACACTTA GGAACACTTN CNACGAGGGG	1860
GTGGAAGAAG AGCAAGGAGC CAGCTGAGGA GAATGAGTGT GGTGGAGAA CCACCACAGC	1920
NCAGGGTCGC CAGANCTGAG GAAGGGGAGG GAAGCTTATC GAGKAMSGWC RACMKCGAGT	1980
TGGCAGGGAT	1990

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 736 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTA CTCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180

TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCC GGCTGG ACTTTTGAG	300
GTTCCCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCCGA AGTTGCTGTG CCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AAACCTACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCACC AGCAGAAATGG GGAATGGAGA GGTGGGCAGG GGTTCAGCT	720
TCCCTTTGAT TTTTGG	736

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCTTCTT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTCAAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAMMGG TTTGWNTCTG NTTAWTGTA TCTATGRAAG TGTTTTTWAT MACAGTATAA	720
TTGTMGTMAC AAAGTTCTGT TTTTCTTTCC CTTTNCAGAA CCTCAAGAGG CTTTGTTTTC	780
TGTGAAACAG TATTTCTATA CAGNTGCTCC AATGACAGAG TNACCTGCAC CGTTGTCCTA	840
CTTCAGAAT GCACAGATGT CTGAGGACAA CCACCTGAGC AATACTGTAC GTAGCCAGGT	900
ACAGCGTCAG TYTCTNAAAC TGCCTYYGNC AGACTGGATT CACTTATCAT CTCCCCTCAC	960



CTCTGAGAAA TGCTGAGGGG GSTAGGNAGG GCTTTCTCTA CTTNACCACA TTTNATAATT	1020
ATTTTTGGGT GACCTTCAGC TGATCGCTGG GAGGGACACA GGGCTTNTTT AACACATAGG	1080
GTGTTGGATA CAGNCCCTCC CTAATTCACA TTTCANC	1117

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT CCTTTAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA	120
TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AACATTAAA CTTTTTTCCT TCGTTAATTC	240
CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGTTTNGTG TCCGAAAGGT CCACTTCGTA TGCTGGTTGA	360
AACAGCTCAG GAGAGAAATG AAACGCTTTT TCCAGCTCTC ATTTACTCCT GTAAGTATTT	420
GGAGAATGAT ATTGAATTAG TAATCAGNGT AGAATTTATC GGGAACTTGA AGANATGTNA	480
CTATGGCAAT TTCANGGNAC TTGTCTCATC TTAAATGANA GNATCCCTGG ACTCCTGNAG	540

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT GCATACTTTG TGTGTCCAGT GCTTACCTGG AATCCNGTCT TTCCCAACAG	60
CAACAATGGT GTGGTTGGTG AATATGGCAG AAGGAGACCC GGAAGCTCAA AGGAGAGTAT	120
CCAAAAATTC CAAGTATAAT GCAGAAAGTA GGTAACYYYY NNTAGATAMN ATCTTGATT	180
TNCAGGGTCA CTGTTATAAG CTAACAGTAT AGNAATGTTT TTATCGTCTT TCTNKGGNCA	240
TAGACTCTN KGAGAATCTC TTGAGAACTA TGATAATGCC CAGTAAATAC NCAGATAAGT	300
ATTTAAGGAG TNCAGATACT CAAANCCCCA CAATACNGTC AAAGCATCCT AGGTAAAGAC	360

AMCNCCTT	AAATACAGAA	TACCAGCATG	GAAAGGTTCA	GGCTGAGGTT	ATGATTGGGT	420
TTGGGTTTTG	GGNNNGTTTT	TTATAAGTCA	TGATTTTAAA	AAGAAAAAAT	AAACTCTCTC	480
CAAACATGTA	AAAGTAAGAA	TCTCCTAAA				509

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 823 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGG	CTAGGTAAAT	GNAAGNTGTT	TAAAGAGAG	ATGNGGNCNG	GGACATAGTG	60
GTACACANCT	GTAATGCTCA	NCACTKATGG	GGAGTACTGA	AGGNGGNSGG	ATCACTTGNG	120
GGTCNGGAAT	NTGAGANCAG	CCTGGGCAAN	ATGGCGAAAC	CCTGTCTCTA	CTAAAAATAG	180
CCANAAWNWA	GCCTAGCGTG	GTGGCGCRCA	CGCGTGGTTC	CACCTACTCA	GGAGGCNTAA	240
GCACGAGNAN	TNCTTGAACC	CAGGAGGCAG	AGGNTGTGGT	GARCTGAGAT	CGTGCCACTG	300
CACTCCAGTC	TGGGCGACMA	AGTGAGACCC	TGTCTCCNNN	AAGAAAAAAA	AAATCTGTAC	360
TTTTTAAGGG	TTGTGGGACC	TGTTAATTAT	ATTGAAATGC	TTCTYTTCTA	GGTCATCCAT	420
GCCTGGCTTA	TTATATCATC	TCTATTGTTG	CTGCTCTTTT	TTACATTCAT	TTACTTGGGG	480
TAAGTTGTGA	AATTTGGGGT	CTGTCTTTCA	GAATTAACTA	CCTNNGTGCT	GTGTAGCTAT	540
CATTTAAAGC	CATGTACTTT	GNTGATGAAT	TACTCTGAAG	TTTTAATTGT	NTCCACATAT	600
AGGTCATACT	TGGTATATAA	AAGACTAGNC	AGTATTACTA	ATTGAGACAT	TCTTCTGTNG	660
CTCCTNGCTT	ATAATAAGTA	GAAGTGAAG	NAACTTAAGA	CTACAGTTAA	TTCTAAGCCT	720
TTGGGGAAGG	ATTATATAGC	CTTCTAGTAG	GAAGTCTTGT	GCNATCAGAA	TGTTTNTAAA	780
GAAAGGGTNT	CAAGGAATNG	TATAAANACC	AAAAATAATT	GAT		823

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTTNTCCNAA	CCAACTTAGG	AGNTTGGACC	TGGGRAAGAC	CNACNTGATC	TCCGGGAGGN	60
AAAGACTNCA	GTTGAGCCGT	GATTGCACCC	ACTTTACTCC	AAGCCTGGGC	AACCAAAATG	120

AGACACTGGC	TCCAAACACA	AAAACAAAAA	CAAAAAAAGA	GTAAATTAAT	TTANAGGGAA	180
GNATTAAATA	AATAATAGCA	CAGTTGATAT	AGGTTATGGT	AAAATTATAA	AGGTGGGANA	240
TTAATATCTA	ATGTTTGGGA	GCCATCACAT	TATTCTAAAT	AATGTTTTGG	TGGAAATTAT	300
TGTACATCTT	TTAAAATCTG	TGTAATTTTT	TTTCAGGGAA	GTGTTTAAAA	CCTATAACGT	360
TGCTGTGGAC	TACATTACTG	TTNCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	420
TTCCATTAC	TGGAAAGGTC	CACTTCGACT	CCAGCAGGCA	TATCTCATT	TGATTAGTGC	480
CCTCATGNCC	CTGKTGTTTA	TCAAGTACCT	CCCTGAATGG	ACTGNGTGGC	TCATCTTGGC	540
TGTGATTTCA	GTATATGGTA	AAACCCAAGA	CTGATAATTT	GTTTGTCCACA	GGAATGCCCC	600
ACTGGAGTGT	TTTCTTTCCT	CATCTCTTTA	TCTTGATTTA	GAGAAAATGG	TAACGTGTAC	660
ATCCCATAAC	TCTTCAGTAA	ATCATTAATT	AGCTATAGTA	ACTTTTTCAT	TTGAAGATTT	720
CGGCTGGGCA	TGGTAGCTCA	TGCCTGTAAT	CTTAGCACTT	TGGGAGGCTG	AGGCGGGCAG	780
ATCACCTAAG	CCCAGAGTTC	AAGACCAGCC	TGGGCAACAT	GGCAAAACCT	CGTATCTACA	840
GAAAATACAA	AAATTAGCCG	GGCATGGTGG	TGCACACCTG	TAGTTCCAGC	TACTTAGGAG	900
GCTGAGGTGG	GAGGATCGAT	TGATCCCAGG	AGGTCAAGNC	TGCAG		945